WEST

End of Result Set

Generate Collection Print

L3: Entry 2 of 2

File: USPT

Jun 5, 1979

DOCUMENT-IDENTIFIER: US 4157390 A TITLE: Process for vaccine preparation

CLAIMS:

1. A process for the preparation of a <u>vaccine</u> for parenteral administraion to pregnant mammals as a means for reducing the incidence of neonatal diarrhoea, in which process K88a,b/adhesion factor of an enteropathogenic strain of E. coli is adsorbed from a cell-free aqueous solution onto erythrocytes possessing their natural surface characteristics, the ratio of adsorbed K88a,b/adhesion factor to the volume of erythrocytes present being in the range 125 to 800 hemagglutination units per ml, and the composition so formed is rendered storable by the addition thereto of a preservative such as sodium <u>azide</u> or formalin.

.

Q9aqq9 bacillus su P77939 rhizobium s Q9ev50 staphylococ 022640 raphanus sa Q9sb22 oryza sativ Q9riy streptomyce Q9rwh7 oryza sativ Q9fek5 hevea brasi Q9fek5 hevea brasi	0994845 094842 0994843 0913474 091744 091744 091747 09177 09177 09177 09177 09177		016827 homo sapien 09379 rhodococcus 09m502 hellanthus 024107 nicotiana g 022822 caenorhabdi 094987 human coxsa 09j956 human coxsa 09j96 human coxsa 09j97 arabidopsis 02873 caenorhabdi 09j12 arabidopsis 09187 arabidopsis 099x83 drosophila 09j187 arabidopsis 099x83 drosophila 09j976 human coxsa 09j976 human coxsa
2 Q9AQQ9 2 P77939 2 Q9EV50 10 Q22640 10 Q9SR92 10 Q9SR97 10 Q9ZWH7 10 Q9FEKS	10 095W99 10 094EV9 2 094EX3 4 098WT9 6 096K3 10 091875 13 0918V5 10 0978V5 10 090504 10 090504 10 024511 5 018193 5 027487	5 09xV24 5 09xV24 10 098/51 11 099/712 2 059141 16 09KR01 16 09KR01 16 09KR01 16 09KR01 2 06910 2 06910 10 09C5XB 11 09CC5XB 12 09CC5XB 13 09CCFXB 14 09CCFXB 15 09CCFXB 16 09XB99 17 09XB99 18 09XB99 19 09XB99 10 09XB99 11 09XB99 12 09XB99 13 09XB99 14 09XB99 15 09XB99 16 09XB99 17 09XB99 18 09XB99 19 09XB99 10 09XB99 11 09XB99 11 09XB99 12 09XB99 13 09XB99 14 09XB99 15 09XB99 16 09XB99 17 09XB99 18 09XB99 18 09XB99 18 09XB99 19 09XB99 19 09XB99 10 09XB99 10 09XB99 11 09XB99 11 09XB99 12 09XB99 13 09XB99 14 09XB99 15 09XB99 16 09XB99 17 09XB99 18 09XB99 1	4 016827 2 093079 10 0241007 10 0241007 11 0241007 12 094007 12 094007 13 094007 14 096007 15 091007 16 09501 17 09501 18 09501 19 09501 10 09
4834 4984 4982 4982 4982 4982	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	5212 702 524 527 527 536 547 1112 1112 1112 1112 702 701 702 703 703 703 703 703 703 703 703 703 703	1216 492 492 492 107 1127 118 318 318 318 318 318 318 318 127 127 121 121 121 121 121 121 121 121
44444444444444444444444444444444444444	.4444444446 0000000000000000000000000000	00000000000000000000000000000000000000	
71 71 70 70 69 69 69	666 666 667 667 667 667 667 667 667 667	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.00 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	665 666 667 668 668 668 668 668 668 668 668
4.5 Compugen Ltd. Search time 41.42 Seconds (Without alignments) (112 Million cell undates/sec	29 S: 562222		predicted by chance to have a score of the result being printed, total score distribution. Description O92pk5 brassica ju Q92pk5 brassica ju Q95pk7 brassica ju Q95pk1 brassica ju Q95pk1 brassica ju Q95pk7 brassica ju Q95pk7 brassica ju Q95pk7 brassica ju Q95pk7 brassica ju Q99pk7 brassica ju Q99pk7 brassica ju Q99pk7 brassica ju Q91421 sporobolus Q91451 staphylococ Q991451 staphylococ Q991451 staphylococ Q99465 chlamydomon Q22472 chlamydomon Q22472 chlamydomon
GenCore version 4. Copyright (c) 1993 - 2000 Cc protein search, using sw model August 22, 2002, 07:45:22; Se	'GAPVWDDNNVITAG	SPTREMBL_19:* 1: Sp_archea:* 2: Sp_bacteria:* 3: Sp_lungi:* 4: Sp_lungi:* 5: Sp_lunwertebrate:* 5: Sp_lunwertebrate:* 7: Sp_mammal:* 7: Sp_mammal:* 8: Sp_organelle:* 9: Sp_page:* 10: Sp_plant:* 11: Sp_rotebrate:* 12: Sp_virus:* 13: Sp_virus:* 14: Sp_unclassified:* 15: Sp_virus:* 16: Sp_unclassified:* 16: Sp_nacteriap:* 17: Sp_archeap:*	number of results analysis of the analysis of
OM protein - pro Run on:	Perfect score: 157 Sequence: 157 Sequence: 150 Scoring table: BLOSUM62 Gapop 10.0, 0 Searched: 562222 seqs, 1 Total number of hits satisfying Minimum DB seq length: 0 Maximum DB seq length: 20000000 Post-processing: Minimum Match Maximum Maximum Match Listing first	Database :	Result and is derived by and is derived by and is derived by the result ouery look of the result ouer look of the result of the result ouer look of the result of the result ouer look of the result of the

Gaps

. 0

<u>.</u>

RESULT

Q9ZPK5

04444444

```
Mizuno K., Fukuda D., Kakihara M., Kohno M., Ha T.L., Sonomoto K.; "Purification and Gene Cloning of Catalase from Staphylococcus warneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
[1]
 [1]
SEQUENCE.
MEDLINE=92405676; PubMed=1526235;
MEDLINE T.U., Phadnis S., Langenberg W., Yoneda K., Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 505;
                                                                                                                                                      Score 81; DB 2; Length 16;
Pred. No. 1.6e-05;
O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                          "Catalase negative mutants of Helicobacter pylori.";
Eur. J. Clin. Microbiol. Infect. Dis. 11:522-526(1992).
SEQUENCE 16 AA: 1706 MW; A3EA880275367560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.
106AF448457EC1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALARE (EC 1.111.16).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78; DB 2;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                          51.6%; Scor.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IRR002226; Catalase.
Pfan; PFR0199; Catalase; 1.
PRINTS; PR001096; CATALASE.
ProDom; PD000510; CATALASE.; 1.
PROSITE; PS00437; CATALASE.1; UN
PROSITE; PS00438; CATALASE.1; UN
SEQUENCE 505 AA; 58042 MW; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.7%;
ilarity 58.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB045340; BAA97560.1;
HSSP; P42321; 2CAE.
                                                                                                                                                      Query Match 51.6
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                   1 MVNKDVKQTTAFGAPV 16
                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus warneri.
                                                                                                                                                                                                                                   Local Similarity
hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1292;
                                                                Midkiff B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ISK-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      CATALASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ZPK6
Q9ZPK6;
                                                                                                                                                                                                                                                                                                                                            09KW19;
                                                                                                                                                                                                                                                                                                                            Q9KW19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISK-1.
                                                                                                                                                                                                                                                                                               m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                             09KW19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q92PK6
    g
                                                                                                                                                                                                                                                                                                                              HD DDT ACCOOC OCCOOC OCCO
                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                          human coxsa
human coxsa
human coxsa
                                                                             human coxsa
human coxsa
   arabidopsis
                    human coxsa
                                                  coxsa
                                                                human coxsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                      Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                   human
                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY'2000 (TrEMBLrel. 13, Created)
01-MAY'2000 (TrEMBLrel. 13, Last sequence update)
01-MAY'2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CATALASE (FRAGNENT).
Helicobacter pylori (Campylobacter pylori).
Helicobacter:
Froteobacteria; epsilon subdivision; Helicobacter group;
NCBI_TAXID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pua E.C.; "Molecular cloning and expression of catalase genes in Brassica
                091985 H
091982 H
091981 H
091980 H
091918 H
091918 H
091918 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83; DB 10; Length 492;
Pred. No. 0.00035;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ide; Iron; Oxidoreductase; Peroxidase.
56946 MW; EA6C455E40E045AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERSIZE (BY SIMILARITY)
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AF104454; AAD17936.1; -.
                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 AA
                                                                                                                                                                                                      ALIGNMENTS
                                             097982
097981
097980
097989
097987
097985
                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P00432; 4BLC.
InterPro; IPR002226; Catalase.
Ffam; PP00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 52.9%;
Best Local Similarity 66.7%;
Matches 14; Conservative
   7777777777777777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 TINFGAPVWNNNSSMTVGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heme; Hydrogen peroxide;
SEQUENCE 492 AA; 56946
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
eurosids II; Bra
 4444444444

CCCCCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R512
Q9R512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uncea.
                                                                                                                                                                                                                                                                                            09ZPK5:
                                                                                                                                                                                                                                                                               Q9ZPK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
```

ö

Gaps

.; 0

RESULT **Q9R512**

g

õ

us-09-488-737-2.rspt

Last sequence update) Last annotation update)

Created)

492 AA

PRT;

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                Raphanus sativus (Radish).
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                          radish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q940G2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q940G2
                                                                            Q9M4X3
                                        ø
                                        RESULT
                                                        Q9M4X3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SON NEW YORK NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                      Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROFECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
-!- CATIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AF104452; AAD17934.1;
-- HSSP; P21179; 1CF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Molecular cloning and expression of catalase genes in Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and expression of catalase genes in Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 10; Length 492; Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                          47.8%; Score 75; DB 10; Length 492; 61.9%; Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                             Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56828 MW; 3AD5D73AF1AD7C5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                            InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR000067; CATALASE.
PRODOM: PD000510; CATALASE.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 TTNSGAPVWNNNSSMTVGPRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pua E.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        juncea.";
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                          juncea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9SYT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTXS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
09SYT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
õ
```

```
ö
                                                                                                      Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
-!- AF248491; AAF71742.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY054663, AAK96854.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALASE.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SEQUENCE FROM N.A. Kwon S.-I., An C.-S.; "Characterization and expression of the catalase gene from small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 492;
                                                                                                                                                                                                                                                                                                   HSSP; 221179; 1CE9.
InterPro; IPR002226; Catalase.
InterPro; IPR00199; Catalase.
PRINTS: PR0000510; Catalase; 1.
PROSITE: PS00437; CATALASE.
PROSITE: PS00438; CATALASE.2; 1.
PROSITE: PS00438; CATALASE.2; 1.
Heme: Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56817 MW; 03E38F08D038276E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 10;
Pred. No. 0.0057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.88;
61.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 47.8 Best Local Similarity 61.9 Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
```

```
pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; Catalase; 1.
PROSITE; PS00437; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                  18 TTNAGAPVWKDIEVMTVGPRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.1%;
55.2%;
                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                   Query Match 47.1'
Best Local Similarity 66.7'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.29
watches 16, Conservative
                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MVF213;
      stapfianus.";
                                                                                                                                                                                                                                                                                                   Q9L4S2;
                                                                                                                                                                                                                                                                                     Q9L4S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
Q9RG14
ID Q9RG14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09RG14
                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                          RESULT
Q9L4S2
      RT DR DR KW KW KW
                                                                                                                                                                                          ò
                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                     g
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROFECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AR104451; AAD17933.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 4.5 KDA PROTEIN (FRAGMENT).
Sporobblus stapfianus (Ressurection grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; PACC clade; Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                                                                                                                           Brassica juncea (Leaf mustard) (Indian mustard).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blomstedt C.K., Gianello R.D., Neale A.D., Hamill J.D., Gaff D.F.; Isolation and characterization of cDNAs associated with the onset of desiccation tolerance in the resurrection grass Sporobolus
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                     Pua E.C.;
"Molecular cloning and expression of catalase genes in Brassica
                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
  47.8%; Score 75; DB 10; Length 492; llarity 61.9%; Pred. No. 0.0057; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 496 AA; 57411 MW; 23DAA98786DC4E5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.8%; Score 75; DB 10; 61.9%; Pred. No. 0.0057;
                                                                                                                                                   496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AA.
                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002226; Catalase.
                                                        29
                                                                    9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 TINSGAPVWNNNSSMTVGPRG 38
                                                      TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.99
Matches 13; Conservative
                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                Similarity
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=56623;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=3707;
Query Match
Best Local Simi
Matches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                004821;
                                                                                                                                                            Q9ZPK7;
                                                                                                                                                 Q92PK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 004821
                                                                                                                       æ
                                                                                 18
                                                      σ
                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                     092PK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     004821
                                                                               g
                                                        õ
                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanz R., De la Fuente R.;
"Catalase deficiency in Staphylococcus aureus subsp. anaerobius is associated with natural loss of function mutations within the structural gene.";
Microbiology 146.465-475(2000).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC BFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 455 AA; 52618 MW; E29A5B259D642CAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 2; Length 455;
Pred. No. 0.0074;
                                                                                                                                                                                                                                                              Indels
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases. BMBL; Y10785; CAR717571; -.
Interpro; IRP002226; Catalase.
Pfam; PF00199; catalase; 1.
Hypothetical protein.
NON_TER
SEQUENCE 41 AA: 4499 WW; 51046FE68DFD2EDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEROXIDE (BY SIMILARITY).
-!-CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
EMBL; AJ000471; CAB76840.1; -.
HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
Bacteria: Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                              47.1%; Score 74; DB 10; 66.7%; Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanz R.;
Thesis (1998), UNIV COMPLUTENSE MADRID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSQQDKKLTGVFGHPVSDRENSMTAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MVF213;
MEDLINE=20170679; PubMed=10708385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
```

S

ö

Gaps

```
PECTES-S. aureus (strain N315), and S. aureus (strain Mu50);

MEDLINE-21311952; PubMed-11418146;

MEDLINE-21311952; PubMed-11418146;

MEDLINE-21311952; PubMed-11418146;

MEDLINE-21311952; PubMed-11418146;

RA Kurda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Aranmori M., Matsumaru H., Maruyama A., Inloue R.-I., Kaito C.,

RA Mizutani-Ui Y., Takhahashi N.K., Sawano T., Inloue R.-I., Kaito C.,

RA Aranmori M., Yamashita A., Oshuma K., Furuya K., Yoshino C., Shiba T.,

RA Aranhisa M., Yamashita A., Oshuma K., Furuya K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

Rattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

Lancet 357:1255-1240(2001)

C. I- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC BFFECTS OF HYDROGEN

DEROXIDE (BY SIMILARITY).

C. I- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.

REMBL, APOU333; BAB42427.1;

REMBL, APOU3335; BAB57496.1;

PREMBL, APOU3332; BAB57496.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heme; Hydrogen peroxide; Iron; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                    ö
  HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74; DB 16; Length 507; Pred. No. 0.0083;
                                                                                                                           Piterru.
Pitan: Pro0199; catalase; 1.
PRINTS; PR00190; catalase.
ProDom; PD000510; catalase.
ProDom; PS00433; Catalase.; 1.
PROSITE; PS00438; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 505 AA; 58324 MW; BEEB05FBB0AEI72F CRC64;
                                                                                                                                                                                                                                                                                                                                                   Ouery Match
47.1%; Score 74; DB 2; Length 505;
Best Local Similarity 55.2%; Pred. No. 0.0083;
Matches 16; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58612 MW; F6B9EE770E2DCBCC CRC64;
  CELLS FROM THE TOXIC EFFECTS OF
                                  2 H(2)O(2) = O(2) + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain Mu50).
Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                             EMBL; AJ000472; CAB76839.1; --
HSSP; P42321; 2CAE.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.18;
55.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6). KATA OR SA1170 OR SAV1334.
                   PEROXIDE (BY SIMILARITY -!- CATALYTIC ACTIVITY: 2 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 47.1
Best Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
  TO PROTECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P42321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxidase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q99UE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099UE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q99UE2
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDT TENERS OF THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                Thomson V.J., Bhattacharjee M.K., Fine D.H., Derbyshire K.M., Figurski D.H., Bhattacharjee M.K., Fine D.H., Derbyshire K.M., Figurski D.H.;

Figurski D.H.;

Direct Selection of IS903 Transposon Insertions by Use of a Broad-Host-Range Vector: Isolation of Catalase-Deficient Mutants of Actinobacillus actinomycetemcomitans.";

J. Bacteriol. 181:7299977307(1999).

J. PROFECTOR: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Catalase deficiency in Staphylococcus aureus subsp. anaerobius is associated with natural loss of function mutations within the structural gene.";
Microbiology 146:465-475(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 484 AA; 54961 MW; D0E523AB2557D8CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEROXIDE (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
EMBL; AF162654; AAF17882.1; -.
                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                          Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 2;
Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thesis (1998), UNIV. COMPLUTENSE MADRID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 12600;
MEDLINE-20170679; PubMed-10708385;
Sanz R., De la Fuente R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P42321; 2CAE.
InterPro; 1PR002226, Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; CATALASE; 1.
PROSITE; PS00437; CATALASE 1:
PROSITE; PS00438; CATALASE 2; 1.
                                                                                                                                                                                                                                                                                                         STRAIN-Y4NAL;
MEDLINE-20042351; PubMed-10572134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.18;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TTAAGAPVVDNDNTMSAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                   actinomycetemcomitans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-ATCC 12600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sanz R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09L4S1
09L4S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09L4S1
ID 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

õ

ö

Gaps

```
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09A009
09A009;
                                                                                                                                                                                                                                   022472;
                                                                                                                                                                                                                        022472
                                                                                                                                                                                                    RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
 DR DR DR SO S
                                                                                                                                                 ŏ
                                                                                                                                                                     g
                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                               Lino-Neto T., Tavares R.M., Palme K., Pais M.S.S.;

"Expression of catalase during senescence and regreening of
Zantedeschia aethiopica spathe.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROPERT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                        Zantedeschia aethiopica (White calla lily).
Skaryyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Zantedeschia.
NCBL_maxID=69721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 73; DB 10; Length 492;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                      Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56968 MW; DC9F3EB1392DEICF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                             PEROXIDE (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALAEE (EC 1.111.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                  492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
         53
                    3 MSQQDKKLTGVFGHPVSDRENSMTAGPRG 31
                                                                                  PRT;
        MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 TINSGAPVWNNNSLTVGARG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                             46.5%;
61.9%;
                                                                                                                                                                                                                                                                                                                  EMBL; AF207906; AAF19965.1;
HSSP; P21179; 1QF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALASE (EC 1.11.1.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3055;
                                                                                                                                                                                                                        TISSUE=LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009484;
                                                                                 09SDS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             009484
                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                       09SDS9
        ò
                           g
                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       â
```

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERAIN=CC-125 WILD TYPE MT+ 137C;
STRAIN=CC-125 WILD TYPE MT+ 137C;
Kim J. Y., Park K.Y., Lee K.O., Lee S.H.;
"Isolation and characterization of a cDNA encoding a catalase from Chlamydomonas reinhardtii (Accession No. AF016902) (PGR 00-016).";
Plant Physiol. 122:293-293(2000).
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                        Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 72; DB 10; Length 493; 61.9%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00199; catalase; 1.
PRINTS; PR00195; catalase.
ProDom; PD000510; catalase.
PROSITE; PS00438; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 493 AA; 55943 MW; 2B74B2BBACCEB773 CRC64;
PRINTS: PRO0199; catalass; 1.
PRINTS: PR00067; CATALASE.
PRODOM; PD000510; CATALASE.1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56227 MW; 3711B90126911C32 CRC64;
                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 \text{ H}(2)0(2) = 0(2) + 2 \text{ H}(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                        Score 72; DB 10;
Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 AA.
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2).
EMBL; AF016902; AAB70006.1; --
HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                           38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 TINSGAPVWNNNSMTVGTRG 38
                                                                                                                                                                                                        Query Match
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN 1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                         18 TINSGAPVWNNNSMTVGTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                099099
ID 099
AC 099
DT 011
DT 011
DE CA
```

```
SEQUENCE FROM N.A.

11 K.-S., An C.-S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raphanus sativus (Radish).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STADING CLAS, STADING CLASTANN-CURED STRAIN CLASS STRAIN-CURED STRAIN CLASS STRAIN-CURED STRAING CLASS STRAING CLASS STADING CLASS SUBMITTER (COTT-2000) to the EMBL/GenBank/DDBJ databases. EMBLs AJ259151; CARE. EMBLSPSP; P42321; 2CARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%; Score 71; DB 2; Length 493; 65.2%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56874 MW; 900B959518A9404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 H(2)0(2) - 0(2) + 2 H(2)0
                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                               Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 AA
                                                                                                                                           493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1: 1.
Oxidoreductase; Peroxidase.
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00199, catalase; 1.
PRINKS; PR00066; CATALASE.
ProDom; PD00510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
  29
                     7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF031318; AAB86582.2; -. HSSP; P21179; 10F7. InterPro; IPR002226; Catalase.
7 KQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 65.2
Matches 15; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                         CATALASE (EC 1.11.1.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     022640;
                                                                                                                                                               Q9EV50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             022640
                                                                                                                                         Q9EV50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
022640
                                                                                                                        09EV50
                                      g
                                                                                                                                              DDT TO DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                           Kwon S., An C.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 483 AA; 54756 MW; 1D423F71AC8CDDBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iron; Heme; Hydrogen peroxide.
); 8C32C77E77828644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEROXIDE.

-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.

-!- COFACTOR: HEME GROUP.

EMBL: U56239; AAA9823.1; -.

HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
              Bacteria; Firmicutes; Bacilius/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 45.2%; Score 71; DB 2; Best Local Similarity 60.9%; Pred. No. 0.023; Matches 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 71; DB 2;
65.2%; Pred. No. 0.023;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                              InterPro: IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; CATALASE. 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interprist 19800226; Catalase.
Fram; PF00199; Catalase; 1.
PRINTS; PR000667; CATALASE.
ProDom; P0000510; CATALASE.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||::|||| |: |||| || 5 KLTTSWGAPVGDNQNSMTAGSRG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UN-2001 (TrEMBLrel, 02, C)
01-UN-2001 (TrEMBLrel, 17, La:
CATALASE (EC 1.11.1.6).
CAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54957 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Peroxidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SNU003;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P77939
P77939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P77939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

œ

```
NCBI_TaxID=1902;
                                                                                     STRAIN-A3(2);
                                                                                                                                            STRAIN=A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSCATC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ZWH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9ZWH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O92WH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                   Iwamoto M., Maekawa M., Saito A., Higo H., Higo K.; "Evolutionary relationship of plant catalase genes inferred from exon-intron structures: isozyme divergence after the separation of monocots and dicots.";
                                                                                                                                                                                                                                                                                                                                                                            Theor. Appl. Genet. 97:9-19(1998).
-i- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Bukaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                      DB 10; Length 491; 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 492;
          Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 491 AA; 56716 MW; 7C20151C3BB16664 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56575 MW; 8C49D4FE45993FC8 CRC64;
                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                            PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; D64013; BAA34204.1; -.
HSSP; P21179; 10F7.
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.6%; Score 70; DB 10
57.1%; Pred. No. 0.033;
tive 4; Mismatches
                                                                                                                                                                         492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 AA.
                                                                           4; Mismatches
                                                   Query Match
Best Local Similarity 60.0%; Pred. No.
Matches 12; Conservative 4; Mismatc
                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00067; CATALASE.
PRODOIT: PR00610; CATALASE.; 1.
PROSITE; PS00437; CATALASE.; 1.
PROSITE; PS00438; CATALASE.2; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 TTNSGAPVWNNNSALTVGERG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                              10 TAFGAPVWDDNNVITAGPRG 29
                                                                                                           01-MAY 2000 (TrEMBLrel, 13, 01-MAY-2000 (TrEMBLrel, 13, 01-DEC-2001 (TrEMBLrel, 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLEEL 13,
01-MAY-2000 (TrEMBLEEL 13,
01-DEC-2001 (TrEMBLEEL 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=LEAF;
                                                                                                                                                                                                                                                                                         NCBI_TaxID-4530;
                                                                                                                                                                         Q9SB22
                                                                                                                                                                                     09SB22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09RJK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RJK9
                                                                                                                                                   RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09RJK9
 SW
                                                                                                ò
                                                                                                                     g
                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OC OS BELL DIT
```

```
ö
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB 2; Length 487;
Pred. No. 0.046;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 487 AA; 55116 MW; 9D3334889EAF60B7 CRC64;
                                                                                                                                                    Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                    STRAIN=A3(2);
Murphy L., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim S., Park S., Lee Y.;
"Cloning and expression of a new rice catalase gene.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB0202021. BAA34714.1; -.
HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 2.
PRINTS; PR00067; CATALASE.
Prodom; PD000510; Catalase; 1.
PROSITE; PS000438; CATALASE_2; 1.
SEQUENCE 492 AA; 56175 MW; A8D3D10D309443F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4530;
```

9

```
[5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             09LDS9;
                                                                                                                                                                                                                                                                                  6SGT60
                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                                                                          09LDS9
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                               à
                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                       Iwamoto M., Maekawa M., Saito A., Higo H., Higo K.;
"Evolutionary relationship of plant catalase genes inferred from exon-
intron structures: isozyme divergence after the separation of monocots
and dicots.";
Theor. Appl. Genet. 97:9-19(1998).
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Malpighiales, Euphorbiaceae, Hevea.
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                            ö
       DB 10; Length 492; 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 69; DB 10; Length 492;
Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ide; Iron; Oxidoreductase; Peroxidase.
56806 MW; B14CE64C275213C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                            PEROXIDE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; D66611; BAA34205.1; -.
HSSP; P00432; 4BLC.
                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA.
                                                                                                                    492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                            Mismatches
        Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hevea brasiliensis (Para rubber tree).
                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                           9 TIAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.98;
      43.9%;
ilarity 57.1%;
Conservative 4
                                                                                                                                               01-MAY-1999 (TrEMBLRELL 10, 01-DEC-2001 (TrEMBLREL 19, CATALASE (EC 1.11.1.6).
                                                                                                                                      01-MAY-1999 (TrEMBLrel, 10, 01-MAY-1999 (TrEMBLrel, 10, 01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 5/.12
Best Local Similarity 5/.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                          Oryza sativa (Rice).
                Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                 NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                               TISSUE-LEAF
        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09FEK5;
                                                                                                                   Q9ZRI9
Q9ZRI9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FEK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
                                                                                               RESULT 24
                                                                                                          Q9ZRI9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09FEKS
                                                                g
                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriuni M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genomic sequence for Arabidopsis thaliana BAC F2D10 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence for Arabidopsis thaliana BAC F5M15 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaverl A.,
Eroriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ecker J.R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ecker J.R.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56705 MW; 73C4361F837EEB8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALAEE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 10;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1013 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                       Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                             InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.3%;
Best Local Similarity 57.1%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 TINSGAPVWNNNSSLTVGARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
```

```
Conservative
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio rumoiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                        CATALASE.
                                                        094EV9
                                                                    094EV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FAZ3
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                           094EV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9FAZ3
                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thanderi A., Toriuni M., Vaysberg M., Yu G., Davis R., Federspiel N.,
A Thaologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
C.-- CATALTATC ACTIVITY: 2 H(2)0(2) - O(2) + 2 H(2)0.
REMBL, ACCOSCS: AAF79625:1; ---
REMBL, ACCOSCS:1.
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUES-STORAGE ROOT,
MEDLINE-21210978; PubMed-11311947;
MEDLINE-21210978; PubMed J., Beeching J.R.;
Reilly K., Han Y., Tohme J., Beeching J.R.;
"Isolation and characterisation of a cassava catalase expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Tremprophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Manihot.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                            Score 68; DB 10; Length 1013;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 67; DB 10; Length 492; 57.1%; Pred. No. 0.093;
                                                                                                                                                                                                                                                                              Oxidoreductase; Peroxidase.
604797360DB8486D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57173 MW; 11C75B456CB6C6F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE CAT1 (EC 1.11.1.6).
Manihot esculenta (Cassava) (Manioc)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-harvest physiological deterioration.";
Biochim. Biophys. Acta 1518:317-323(2001).
EMBL; AF170272; AAD50974.1; -.
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002226; Catalase.
Pfam; PR00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
Oxidoreductase; Peroxidase.
                                                                                                                                                                                  HSSP; P00432; 4BLC.
InterPro; 1PR00226; Catalase.
InterPro; PR00199; catalase; 2
PRINTS; PR00067; CATALASE.
PRODM; P0000510; Catalase; 2.
PROSITE; PS000437; CATALASE.1; 2.
PROSITE; PS00438; CATALASE.1; 1.
                                                                                                                                                                                                                                                                              ide; Iron; O
116681 MW;
                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                         539 TINSGAPVWNNNSSLTVGTRG 559
                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 43.3%;
Best Local Similarity 57.1%;
Matches 12; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.7
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                           Heme; Hydrogen peroxide; SEQUENCE 1013 AA; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66MS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66MS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09SW99
                                                                                                                                                                                                                                                                                                                                                                                                         g
     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ichise N., Morita N., Hoshino T., Kawasaki K., Yumoto I., Okuyama H.; "Cloning of the Complete Catalase Gene from the Hydrogenperoxide-resistant Bacterium Vibrio rumoiensis S-1 and Its Subcelluar localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                              Suaeda maritima subsp. salsa.
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.
NCBI_TaxID=126914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=76258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.7%; Score 67; DB 10; Length 492;
Best Local Similarity 57.1%; Pred. No. 0.093;
Matches 12; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Wang P.P., Ma C.L., Sun Y.F., Zhao Y.X., Zhang H.;
Wang P.P., Ma C.L., Sun Y.F., Zhao Y.X., Zhang H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF304210; AAK67359.1; -
SEQUENCE 492 Aa; 56788 MW; 8532135DE66DA3B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB030821; BAB12412.1; -.
HSSP; P42321; 2CBE.
InterPro; IRR002226; Catalase.
Pram; PF00199; catalase; 1.
ProDom; PB00057; CATALASE.
ProDom; PB00057; CATALASE.
PROSITE; PS000437; CATALASE.1; UNKNOWN_1.
SEQUENCE 509 AA; 57659 MW; CE3A2B4FDIC7DEE8 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%; Score 66; DB 2;
61.9%; Pred. No. 0.14;
Live 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 TANSGAPVWNNNNSLTVGHRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FAZ3;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
CATALASE VKTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || |||||| : :|||||||
14 TIDFGAPVVINRDSLTAGPRG
```

us-09-488-737-2.rspt

```
0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 AA.
                                                                                                                                        493 AA.
                    41.4%; Score 65; DB 61.9%; Pred. No. 0.2; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis (serogroup A), and Neisseria meningitidis (serogroup B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE-20222556; PubMed=10761919;
                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                         PRT;
                                                               29
                                                                          28 TTGGGNPIGDKLNVMTAGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TTKTGQPVWNDDSSLTVGARG
                                                             9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALASE (EC 1.11.1.6).
KATA OR NMA0050 OR NMB0216.
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                        PRELIMINARY;
                                                                                                                                                              (TrEMBLrel.
                             Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=ROOT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                             01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JRF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JRF5
                                                                                                                                        081337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
Q9JRF5
                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                RESULT
081337
                                                                                   g
                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C STRAIN-BREED BEAGLE;
MEDLINE-20579473; PubMed-11137458;
MEDLINE-20579473; PubMed-11137458;
Makamura K., Watanabe M., Takanaka K., Sasaki Y., Ikeda T.;
Makamura K., Watanabe M., Takanaka K., Sasaki Y., Ikeda T.;
T nucleotide substitution leading to thermal-instability and enhanced proteolysis of mutant enzyme."; 1 Int. J. Blochem. Cell Biol. 32:1183-1193(2000).

R EMBL; AB038231; BAB20764.1; -.
R HSSP; PO0432; ABLC.
R InterPro; IPR003226; Catalase.
R Pfam; PF00199; catalase; 1.
R PRINTS; PR00067; Catalase; 1.
R PRINTS; PR0006510; Catalase; 1.
R PROSTITE; PS00437; CATALASE.
R PROSTITE; PS00437; CATALASE.
R PROSTITE; PS00437; CATALASE.
R PROSTITE; PS00437; CATALASE.]; 0.
                                                                                                                                               Gaps
                                                                                  Homo saplens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                         Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 527 AA; 59733 MW; 637A97F24FFF1E15A CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Length 527;
                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   DB 4;
0.14;
                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 4
Pred. No. 0.14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    527 AA
          527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                               Created)
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                         InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR000067; CATALASE.
PROSUM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                         28 TTGAGNPVGDKLNVITVGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                           9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                   42.0%;
                             01-JUN-2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-DEC-2001 (TrEMBLrel, 19, CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC.
Canis familiaris (Dog).
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09GKY3;
                     09BWT9;
          Q9BWT9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GKY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
Q9GKY3
09BWT9
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Michalowski C.B., Quigley-Landreau F., Bohnert H.J.;

Michalowski C.B., Quigley-Landreau F., Bohnert H.J.;

T "Different isoforms of catalase are expressed in leaves and roots of the common ice plant.";

T the common ice plant.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

R HSSP; P21179; 1CF9.

R HSSP; P21179; 1CF9.

R PRINTS; PR000225; Catalase.

R PRINTS; PR00067; CATALASE.

R PRINTS; PR00067; CATALASE.

R PROSTIE; PS000437; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699, 491;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ROOT CATALASE (EC 1.11.1.6).
Mesembryanthemum crystallinum (Common ice plant).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Caryophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%; Score 64; DB 10; Length 493; 52.4%; Pred. No. 0.27;
Length 527;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
9
                                                                           9
       DB 6;
```

```
InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR000067; CATALASE.
PRODOM; PD000510; CATALASE.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                             9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                             28 TTGAGVPIGDKLNAMTAGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TTEAGAPVVDNQNSMTAGARG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-DEC-2001 (TrEMBLrel. 19, CATALASE ISOZYME.
                                                                                    Query Match
Best Local Similarity 57.1:
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=PM70;
                                                                                                                                                                                                                                                                                                                                                              Plasmid pAM10.6.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HKTE OR PM0032
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CB36
                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                             P77924
P77924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9CPK5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
09CPK5
  DR
DR
SO
                                                                                                                                                                         g
                                                                                                                                                                                                                                                            g
                                                                                                                                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                              AEDINE-2017575; PubMed=10710307;
MEDLINE-2017575; PubMed=10710307;
MEDLINE-2017575; PubMed=10710307;
Bisen J.A., Ketchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E.,
Bisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Pelsischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Gotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PROXIDE (EW SIMILARITY).
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
EMBL: AF170069; AAF89686.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Grundy M.A.; Gerhard G.S., Kauffman E.J., Grundy M.A.; Molecular cloning and sequence analysis of the Danio rerio catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii: Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Whitehead S., Spratt B.G., Barrell B.G.;
Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 16; Length 504; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Peroxidase; Complete proteome.
SEQUENCE 504 AA; 57167 MW; 26858B47446F3775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comp. Biochem. Physiol. 127:447-457(2000).
                                                                                                                                                                                                                                                                                                                                                       PRINTS: PRODO67; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; UNKNOWN_1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                        Science 287:1809-1815(2000).
EMBL; AL162752; CAB83367.1; -.
EMBL; AE002379; AAF40672.1; -.
                                                                                                                                                                                                                                                                                                                               InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZFIN; ZDB-GENE-000210-20; cat.
InterPro: IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||| |: | :||||||
16 GAPVADNQNSLTAGPRG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 GAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 40.8
Best Local Similarity 70.6
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00199; catalase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                    HSSP; P42321; 2CAE.
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P00432; 4BLC
                                                                                                                                                                                                                                                                                                                   NMB0216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0918V5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q918V5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0918V5
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peters M., Heinaru A., Nurk A.; "Plasmid-encoded catalase KatA, the main catalase of Pseudomonas fluorescens strain Cb36."; FEMS Microbiol. Lett. 200:235-240(2001). EMBL; U72068; AABI7009.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                       40.8%; Score 64; DB 13; Length 526; 57.1%; Pred. No. 0.29;
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 526 Aa; S9542 MW; 9FA05D42737662A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.5%; Score 62; DB 2; Length 506; 61.9%; Pred. No. 0.55;
                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 AA; 57324 MW; F1EAA728C5D41CBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               506 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AA
                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21318967; PubMed=11425481;
```

```
Helianthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3544;
 Heliantheae, He
NCBI_TaxID=4232
                                                                                                                                                                                                                                                                                                                                                                       RESULT
081336
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Welssenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis ILIA03." Genome Res. 11:731-753(2001).
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
         May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL, AE006036; AAK02116.1;
                                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                    ;
0
                                                                                                                                                             38.9%; Score 61; DB 16; Length 484; 47.6%; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60; DB 16; Length 349;
Pred. No. 0.73;
                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
                                                            Interpro; IPR002226; Catalase.
Pfam: PF00199; catalase; 1.
PRINTS; PR00057; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
Complete protecome.
SEQUENCE 484 AA; 55127 MW; 5BE648D3610A6420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 349 AA; 37380 MW; 4A71A677ECE3D3A4 CRC64;
                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.111.1.6).
                                                                                                                                                                                                                                                                                    349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-IL1403;
MEDLINE-21235186; PubMed-11337471;
MEDLINE-21145866; PubMed-11248100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KQTTAFGA--PVWDDNNVITAGP 27
                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                     38.2%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006267; AAK04397.1;
                                                                                                                                                                        Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                    HSSP: P42321: 2CAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9M504
Q9M504;
                                                                                                                                                                                                                                                                                  09CIQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                             RESULT
Q9CIQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                             ò
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-CV. SPANNERS ALLZWECK; TISSUE-COTYLEDONS;

Heinze M., Baur B., Eising R.;

Heinze M., Baur B., Eising R.;

Biogenesis of catalase forming the crystalline inclusions in peroxisomes of sunflower cotyledons ";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN SERVES TO SIMILARITY).

C. 1- CATALYTIC ACTIVITY: 2 H(2)0(2) - O(2) + 2 H(2)0.

EMBL; AF243517; AAF61732.1; - O(2) + 2 H(2)0.

RMSD; POOQA32; HBLC.

SEMBL; AF243517; CATALASE.

PROSTIE: PRO0065; CATALASE.

PROSTIE: PS00433; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 10; Length 492;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heme, Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56931 MW; AADF2B516C130163 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 492 AA; 56886 MW; 6DD5DBOAFAAD5C60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ς.
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat CATALASE (EC 1.11.1.6).
Mesembryanthemum crystallinum (Common ice plant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
37.6%; Score 59; DB 10;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 7; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PRODOGT; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.6%;
Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TINYGAPVYNNDSSLTVGTRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
```

```
TRAIN—EATCCIOL47;

X MEDLINE—97334128; Pubmed—9190825;

X MEDLINE—97334128; Pubmed—9190825;

X Cho Y.H., Roo J.H.;

I solation and expression of the catA gene encoding the major

RT vegetative catalase in Streptomyces coelicolor muller.";

J. Bacteriol. 179:4049-4052(1997).

L. SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN

ENCORTE (BY SIMILARITY).

C. !- CATALITIC (BY SIMILARITY).

C. !- CATALIASE.

DR FRINTS; PRO00507; CATALASE.

DR PRINTS; PRO00507; CATALASE.

DR PROSITE; PS00437; CATALASE.

DR PROSITE; PS00438; CATALASE.

SEQUENCE 488 AA; 55440 MM; 323633B73E46C7C8 CRC64;
                                                                                                                                                                                                                                        Streptomyces coelicolor.

Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBL_MAND-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.9%; Score 58; DB 2; Length 488; Best Local Similarity 46.2%; Pred. No. 2.1; Matches 12; Conservative 3; Mismatches 11; Indels
                                                                                                                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CATALASE (EC 1.11.1.6).
                                                                                                                      488 AA.
                                                                                                                      PRT;
9 TTAFGAPVWDDNNVITAGPRG 29
                   || || ||||:::|: :| || || || TINSGAPVYNNNSSLIVGIRG 38
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                  P77948
P77948;
                                18
                                                                                    RESULT
P77948
δλ
                                                                                                                      g
```

Search completed: August 22, 2002, 07:45:26 Job time: 145 sec

3 NKDVKQTTAFGAPVWDDNNVITAGPR 28

à qq

; 0

Gaps

Run

```
097pv3 streptococc 09f9s8 edta-degrad 09rg53 streptovert 09139 streptomyce 09x438 leptospira 09x691 coxiella bu 092596 rhizobium m 092ef8 oryza sativ 09raj9 moraxella s
                                                                 099w61 staphylococ
091yd8 prototheca
096c2p1 neurospora
040450 nicotiana s
09axu2 pelargonium
093y56 arabilopsis
043364 nicotiana s
095tv3 drosophila
096g7 drosophila
096g7 drosophila
096g7 drosophila
096g7 drosophila
098g9 xylella fas
09g196 candidatus
02g14 toxoplasma
09tm9 toxoplasma
                                                                                                                                                              O92191 arabidopsis 09206 arabidopsis 09206 arabidopsis 09102 cae mays (m 019072 caenorhabdi 098491 mycopłasma 033451 elmeria ten 025820 plasmodium 094477 drosophila 095513 loofah witc 09791 thermoplasm 095638 methanococc 093638 methanococc 093638 methanococc 093638 methanococc
                                                                                                                                                                                                                                             0980a5 sulfolobus
0975n8 sulfolobus
0976135 caenorhabdi
0976135 caenorhabdi
097615 ulfolobus
02509 hydra magni
029514 archaeoglob
099915 yarrowia li
083774 stigmatella
082788 blastocysti
                                                                                                                                                                                                                                                                                                                      Q47012 arabidopsis
94009 arabidopsis
94009 arabidopsis
94007 arabidopsis
92769 malus domes
97569 incottana t
99759 arabidopsis
039093 arabidopsis
03400 arabidopsis
094000 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                            091n13 arabidopsis
042336 arabidopsis
049736 arabidopsis
09k713 bacillus ha
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9hpe4 halobacteri
045622 caenorhabdi
091rq9 sus scrofa
09n9d5 scoliopteri
Q9na07 drosophila
064490 arabidopsis
Q9zv47 arabidopsis
                                                       Q9cei0 lactococcus
Q9tlv8 cyanidium c
                                                                                                                                            Q26114
Q9TMM9
Q78325
Q9ZT91
Q39206
Q9FUZ6
                                                                                                                                                                                                                                                                                                                                                                                           209LN13
Q42336
Q42336
Q49736
Q9K7L3
Q9HPE4
                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TRQ9
Q9N9D5
Q9NA07
O64490
Q9ZV47
                                                       Q9CEI0
Q9TLV8
Q99W61
                                                                         Q9TJQ8
Q9C2P1
Q40450
Q9AXU2
Q93X56
Q43364
Q95TV3
Q9V6Q7
Q9P9Q9
                                                                                                                                                                                                                                                                076135
P91150
Q976B1
Q25099
029514
                                                                                                                                                                                                                                                                                                                        242012
P94009
P94000
P94007
Q92RP9
Q9C5L4
Q39093
Q94AD0
Q94AD0
Q97PV3
Q9F9S8
Q9RG53
                  Q93T39
Q9XG31
Q9X6G1
Q925Y6
Q9SEF8
Q9RAJ9
                                                                                                                                                                                  Q19072
Q98QG1
Q33451
Q25820
Q9V4M7
Q9S513
Q97511
Q93638
                                                                                                                                                                                                                                               Q980A5
Q975N8
                                                                                                                                                                                                                                                                                                            082788
                                                                                                                                                                                                                                                           Q9HNK9
                   & & & & & O
 Q9kv37 vibrio chol
Q9kv37 vibrio chol
Q9k126 vibrio chol
Q9k117 neisseria m
Q9k117 neisseria m
Q9k120 porphyromon
Q9rhi1 porphyromon
Q9k110 porphyromon
Q9k10 porphyromon
Q9k10 porphyromon
Q9k10 porphyromon
                                                                                                                                                                                                                                                                                                                                                                                                                                 0999m0 caulobacter
0933r9 ureaplasma
0929w4 rickettsia
09r955 streptomyce
09hwd3 pseudomonas
                                                                                                                                                                                                                                                                                                                                                               Q97eh5 clostridium
                                         2002, 07:43:01; Search time 41.42 Seconds (without alignments) 91.885 Million cell updates/sec
                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                   Description
       4.5
Compugen Ltd
                                                                                                                           hits satisfying chosen parameters:
                                                                                                              562222 seqs, 172994929 residues
      GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                22
                                                                                                                                                                       summaries
                              - protein search, using sw model
                                                                               1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                          09KUZ6
092716
09K117
09JR15
09R420
09RH12
09RH11
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q933R9
Q92GW4
Q9RG55
Q9HWD3
                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                  0990M0
                                                                                                                                                                                                         sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                        sp_unclassified:*
                                                                                                                                                                                                                                                           sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                              sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 100
                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
                                                                                                                                       seq length: 0
seq length: 200000000
                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                          sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                   10000
                                                                                                                                                                                                                                                                                                                                                                                                                                         16
16
16
                                                                                                                                                                                                                                                                                                                                                               10
10
10
10
                                                                                                                                                                                                                                                    sp_rodent:*
                                                                   US-09-488-737-1
                                                                                                                                                                                                                                               sp_plant: *
                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                    *: fundf-ds
                                                                                                                                                                                   SPIREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                              August 22,
                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                    uua0000000000uuuu
                                                                                                                                                                                                                                               ..
9
                                                                                                                                                          Post-processing:
                                                                                                                           Total number of
                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                    1111
1111
1109
1107
1107
1107
1106
1106
1106
                                                                                            Scoring table:
                                                                                                                                       Minimum DB
Maximum DB
                                OM protein
                                                                                 Sequence:
                                                                                                               Searched:
                                                                                                                                                                                   Database
                                            :
o
```

Result Š. ~

```
SEQUENCE FROM N.A.
STRAINEL TOW NIG661 / SEROTYPE 01;
MEDLINE=1 TOW NIG661 / DEBOTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINEL TOR NIS961 / SEROTYPE 01;
MEDLINE-21 TOR NIS961 / SEROTYPE 01;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Hodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Ummayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                        Nature 406:477-483(2000).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AE004120; AAF93494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AE004124; AAF93535.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                            "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111; DB 16; Length 394;
                                                                                                                                                                                                                                                                                                                                         43185 MW; A047E398A84B8A40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF0DE31A00618B36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 111; DB 16; 90.5%; Pred. No. 8.5e-10; iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                             InterPro; IPR000795; GTP_EFTU.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Complete proteome; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP: 1.
COMPLETE PTCHOME; GTP-binding.
SEQUENCE 394 AA; 43126 MW; BF(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.5 ses 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELONGATION FACTOR TU
                                                                                                                                                                                                                                                    HSSP; P02990; 1ETU.
TIGR; VC0321; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02990; 1ETU.
TIGR; VC0362; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                             Complete | SEQUENCE
                                                                                                                                                                                              cholerae.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KUZ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9KUZ6
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q9KUZ6
   OX
RRY
RRA
RRA
RRA
RRI
RRI
RRI
RRI
DR
RW
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9d791 mus musculu
Q9nar5 clytus arie
Q9nft8 scoliopteri
Q9nf03 clytus arie
Q9vfa6 drosophila
Q9nfu1 drosophila
Q9nfu1 drosophila
Q9nfu2 scoliopteri
Q9n6u2 clytus arie
Q9n6u0 leptinotars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    AN SEQUENCE FROM N.A.

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE-21393925; PubMed=11466286;

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Tatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Tatsov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Datesium Clostridium acctobutylicum.";

RT "Genome sequence and comparative analysis of the solvent-producing

RT Bacteriol. 183:4833-4838(2001).

RE EMBL; AE007809; AAK81075.1; ...

DR InterPro; IPR004161; GTP_EFFU.

DR InterPro; IPR004161; GTP_EFTU.D3.

InterPro; IPR004160; GTP_EFTU.D3.
                leptinotars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
Gacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
               09n9w0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.1%; Score 112; DB 16; Length 397; 95.2%; Pred. No. 5.9e-10; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU, 1.
PRINTS; PR00315; ELONGATNFCT.
COMPLETE, PS00301; EFACTOR_GTP; 1.
SEQUENCE 397 AA; 43452 MW; F031B2F700434452 CRC64;
                                                                                                                                                                                                                                                                                            (Trembirel. 18, Created)
(Trembirel. 18, Last sequence update)
(Trembirel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA.
                                                                                                                                                                                                                                                                  397 AA
                                                                                                                                                                                           ALIGNMENTS
             09009W0
09D791
090AR5
0906T8
0906U3
090VFA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                 Q9N6T9
Q9N6U2
Q9N6U0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KEKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                       ELONGATION FACTOR TU (EF-TU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19, ELONGATION FACTOR FU.
                                                                                                                                                                                                                                                                                                                                                                      Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                           01-OCT-2001 (
01-OCT-2001 (
01-DEC-2001 (
 Query Match
                                                                                                                                                                                                                                                              Q97ЕН5
Q97ЕН5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KV37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09KV37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                     RESULT
Q97EH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q9KV37
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

ö

Gaps

ö

Indels

Length 394;

```
P02990; 1EFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9JRI5
Q9JRI5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
Q9JRI5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
MEDLINE=201755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Charabotty T.,
Charabit A., Chetounani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hahn T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                      ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 AA; 43353 MW; CEOFA4906D644C24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.6%; Score 109; DB 16; 90.5%; Pred. No. 1.8e-09; ive 2; Mismatches 0;
  Pred. No. 8.5e-10;
                                                                                                                                                                                                   395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AA
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSLATION ELONGATION FACTOR IU.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR 6A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294:849-852(2001).
EMBL; AL596173; CAC98028.1; -.
ListiList; LIN02802; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                              90.5%;
                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                          2 KEKFNRTKPHVNIGTIGHVDH
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11679669;
                                                                                                                                                                                                                                                                                                                       FUFA OR LIN2802.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                      UFA PROTEIN
                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMB0139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9K117
Q9K117;
                                                                                                                                                                                             092716
                                                                                                                                                                                                                        092716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      വ
                                                                                                                                                             4
                    Matches
                                                                                                                                                             RESULT
Q92716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID DT TO DT 
                                                                                                                                                                                                                        õ
                                                            à
                                                                                               g
```

```
SEQUENCE FROM N.A.
STRAIN=MC58 / SEROGROUP B;
STRAIN=MC58 / SEROGROUP B;
MEDLINE=2017555; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Matte D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Scallato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup A), and
Neisseria meningitidis (serogroup B).
Bacteria: Proteobacteria: beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=65699, 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. EMBL, AL16275; CAB83449.1; -. EMBL, AC002371; AAR40583.1; -. EMBL, AL162752; CAB83464.1; -.
                                                                                                                                                                                                                                           Science 287:1809-1815(2000).
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AE002372. AAF40598.1; -.
HSSP; P02990; IETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Z2491 / SEROGROUP A / SEROTYPE 4A;

MEDLINE-20225565 Pubmed-10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%; Score 107; DB 16; Length 394; 85.7%; Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TU (TRANSLATION ELONGATION FACTOR TU).
(TUTPAL OR NMA0134 OR NMB0124) AND (TUFAZ OR NMA0149).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Complete protecome; Elongation factor; GTP-binding.
SEQUENCE 394 AA; 42925 MW; 55762F03EC048563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KEKFERSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000795; GTP_EFTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis 2249
                                                                                                                                                                                                                                                                                                                                                                                                                NMB0139;
```

```
STRAIN-FDC 381;
A Nagai A., Itoh N.;
A nagai A., Itoh N.;
Ber-Tu sequence of Porphyromonas gingivalis.";
L schmitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035461; BAA88134.1; -.
R HSSP; PO2990; IEFU.
R InterPro; IPR004161; GTP_EFTU_D2.
R InterPro; IPR004161; GTP_EFTU_D3.
R InterPro; IPR004161; GTP_EFTU_D3.
R Pfam; PF03144; GTP_EFTU_D2; 1.
R Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO004161; GTP_EFTU_D2.
InterPro; IPRO004161; GTP_EFTU_D3.
Pfam; PP00009; GTP_EFTU_1.
Pfam; PP03144; GTP_EFTU_1.
Pfam; PR03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                    PRINTS; PR00315; ELONGAINECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KEHFNRSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KEHFNRSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.09
Best Local Similarity 85.79
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SUNY 1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP-binding
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9RHI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EF-TU.
EF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q9RHI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q9RHI0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDT SOOCCOOR BEACT OF THE SOOCCOOR SOOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ă
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, CFB group, Bacteroidetes; Bacteroidales; Porphyromonadaceae;
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                       Query Match

87.0%; Score 107; DB 16; Length 394;
Best Local Similarity 85.7%; Pred. No. 3.8e-09;
Matches 18; Conservative 2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%; Score 107; DB 2; Length 395;
85.7%; Pred. No. 3.8e-09;
tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A7A1 28, AND W83;
Magai A., Itoh N.;
Magai A., Itoh N.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EEMBL; A8003464; BAA88137.1; -.
EEMBL; A80035462; BAA88135.1; -.
HSSP; P02990; IEFU.
TIGR; NMB0124; -.
InterPro; IPR000795; GTP_EFTU.
PRINTS; PR00315; ELONGATNRCT.
PROSITE; PS00310; EFETU.
COMPLETE POTCHORGER: BLONGATION factor; GTP-binding.
SEQUENCE 394 AA; 42909 WW; 0C571C3D20CBE944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA; 43699 MW; 19FCECD3189BCF3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03143; GTP_EFTU_D3; I.
PKINTS; PR00315; ELCNOATNECT.
PROSITE; PS00301; EFACTOR_GTP; I.
                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                       3 KEKFERSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KEHFNRSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.0 Best Local Similarity 85.7 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09RHI2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RHI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                  Q9R420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RHI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
    ò
```

ö ö Porphyromonas gingivalis (Bacteroides gingivalis). Bacteria, CFB group; Bacteroidetes; Bacteroidales; Porphyromonas. Porphyromonas. NCBL_TaxID=837; Gaps Gaps ó ő 87.0%; Score 107; DB 2; Length 395; 85.7%; Pred. No. 3.8e-09; tive 2; Mismatches 1; Indels Length 395; Nagal A., Itoh N.; Nagal A., Itoh N.; "EF-Tu sequence of Porphyromonas gingivalis."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB035463; BAA88136.1; -. HSSP; P02990; 1EFU. 395 AA; 43655 MW; 1F284BA6154DA84A CRC64; 395 AA; 43727 MW; B02F39D3173ADA3D CRC64; 01-WAY-2000 (TrEMBLrel. 13, Created) 01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 87.0%; Score 107; DB 2; 85.7%; Pred. No. 3.8e-09;

```
87.0%; Score 107; DB 2; L
85.7%; Pred. No. 3.8e-09;
iive 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA.
                                                                                                                            396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                              22
                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KEKFERTKPHCNIGTIGHVDH 23
                                                          3 KEHFNRSKPHVNVGTIGHVDH
                                              2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 87.0
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
           Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                           CC3199 AND CC1240.
                                                                                                                                                                                                                                       NCBI_TaxID=69394;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CC1240;
                                                                                                                        Q99QM0;
Q99QM0;
01-JUN-2001 (
                                                                                                                                                                                                                             Caulobacter
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q933R9
Q933R9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                   RESULT
Q99QM0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0933R9
                                              ð
                                                                  g
                                                                                                                                     δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                            Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteroides forsythus.
Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                "EF-Tu sequence of Porphyromonas gingivalis.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB035465; BAA88138.1; -.
R HSSP; P02990; IEFP.
R InterPro; IPR000795; GTP_EFTU.
R InterPro; IPR004160; GTP_EFTU.
R InterPro; IPR004160; GTP_EFTU.
R Pfam; PF00009; GTP_EFTU_D3.
R Pfam; PF03144; GTP_EFTU_D2; 1.
R Pfam; PF03144; GTP_EFTU_D2; 1.
R Pfam; PF03143; GTP_EFTU_D2; 1.
R PRINTS; PR00315; ELONGATNFCT.
R PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                  87.0%; Score 107; DB 2; Length 395;
85.7%; Pred. No. 3.8e-09;
.ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 43037;
Nagai A., Itoh N.;
"EF-Tu sequence of Bacteroides forsythus.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035466; BAA88139.1; --
HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 AA; 43695 MW; 440B33AEE8F39CEF CRC64;
                                                                                                                                                                                                                                                                                                                 395 AA; 43669 MW; 1F2F39D3173ADA3F CRC64;
                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00301; EFACTOR_GTP; 1. GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                          3 KEHFNRSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 18; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                        [1]
SEQUENCE FROM N.A.
STRAIN=ATCC 33277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                        Nagai A., Itoh N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-28112;
                                                                                                              NCBI_TaxID-837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteroides.
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           о9кнн9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09RHH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EF-TU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                09кнн9
ò
                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO 19089 / CB15;

MEDIINE-21175698; PubMed-11259647;

Micran W.C., Feldblyum T.V. Laub M.T., Paulsen I.T., Nelson K.E.,

Risen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Betocka I., Nelson W.C., Newton A., Stephens C., Phacke N.D., Ely B.,

Potocka I., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

M. Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

M. Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

1. SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

REMBL, AE005804; AAK23161.1;

REMBL, AE005809; LETU.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 396;
Length 395;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000795; GTP_BFTU.
InterPro; IPR0004161; GTP_BFTU_D2.
InterPro; IPR0004160; GTP_BFTU_D3.
Pfam; PF00009; GTP_BFTU_D3.
Pfam; PF03143; GTP_BFTU_D3; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
COMPILE; PS00301; EFACTOR_GTP; 1.
COMPILE; PS00304; EFACTOR_GTP; 1.
COMPILE; PS00304; ENGRATHOR factor; GTP-binding.
SEQUENCE 396 AA; 43339 MW; IF58829078B624D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSLATION ELONGATION FACTOR EF-TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ELONOATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 107; DB 16; 90.5%; Pred. No. 3.8e-09;
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE 15692 / PAO1;

MEDINRE-2043337; PubMed-1, Mizoguchi S.D., Warrener P., Atover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Actover C.K., Park M. S.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., As Mith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).

I. SIMILARIY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY. BE MISP; PO2990; 1EFC.

HISP; PO2990; 1EFC.

RISP; PO2990; 1EFC.

RICKLEFPLO, 1PRO00795; GTP EFTU.
                                                Streptomyces mobaraensis.
Bacteria; Firmioutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                          STRAIN-ATCC29032;
Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
Elengation factor Tul from the pulvomycin producer Streptcomyces
mobaraense is resistant to both pulvomycin and kirromycin.";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
HSSP; P02990; IETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.2%; Score 106; DB 2; Length 39
90.5%; Pred. No. 5.6e-09;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00315; ELONGATNECT.
PROSTITE; PS00301; BFACTOR_GTP; 1.
Complete proteome; GTP-binding and angle proteome; A397 AA; 43369 MW; A019D5BF8BBAB942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 AA; 43811 MW; DA439151BFE6BC2E CRC64;
   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGAINFOT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                    ELONGATION FACTOR TUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELONGATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TUFA OR PA4265
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSC
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9HWD3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9HWD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HWD3
   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).

EMBL: AE008652; AAL03546.1; -.
CCMplete proteome.

SEQUENCE 394 AA; 42868 MW; IFBE465785530C63 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%; Score 106; DB 16; Length 394; 90.5%; Pred. No. 5.6e-09; ative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                              Length 394;
                                                                                  Kong F., Gilbert G.L.; "Genomic based mapping and sequencing of U. parvum and U.
                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF270767; AAK58630.1; -.
EMBL; AF270758; AAK58621.1; -.
                                                                                                                                                                                                                                                                                                                                      4CB4B2D776A5B145 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                            Score 106; DB 2;
Pred. No. 5.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                             AF270760; AAK58623.1; -. AF270761; AAK58624.1; -.
                                                                                                                                                                                            AF270759; AAK58622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                            86.2%;
90.5%;
Mycoplasmataceae; Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KAKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                  SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELONGATION FACTOR EF-TU
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=MALISH 7;
                  NCBI_TaxID=2130;
                                                                                                                         urealyticum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUF OR RC1008
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q92GW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09RG55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92GW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9RG55
                                                                                                                                                                                          EMBL;
EMBL;
                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
Q9RG55
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

q ŏ

δ a AC DT DT

ö

Gaps

.; 0

Length 397;

097PV3; 097PV3

RESULT 17

셤

ð

097PV3

SP1489

```
Liu Y., Loude T.M., Payne J., Bohuslavek J., Bolton H. Jr., Xun L.;
"Identification, purfication, and characterization of iminodiacetate oxidase from the EDTA-degrading bacterium BNC1.";
Appl. Environ. Macrobiol. 67:696-701(2001).
EMBL; AF156664; AAG09263.1; -..
HISSP; PO7157; IAIP.
InterPro; IRR000795; GTP_EFTU.
                                                                                Bohuslavek J., Payne J.W., Liu Y., Bolton H. Jr., Xun L.; "Cloning, Sequencing, and Characterization of a Gene Cluster Involved in EDTA Degradation from the Bacterium BNCI."; Appl. Environ. Microbiol. 67:688-695(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptoverticillium netropsis (Streptoverticillium flavopersicus).
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=55404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsthoorn-Tieleman L.N., Claij N., Hilgenfeld R., Kraal B.;
"Elongation factor Tul from the pulvomycin producer Streptomyces
mobaraense is resistant to both pulvomycin and kirromycin.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF153618; AAF22608.1; -.
HSSP; POS990; LETU.
InterPro; IPRO04795; GTP_EFTU._D2.
InterPro; IPRO04161; GTP_EFTU._D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6B41737CCD77AA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 AA; 43682 MW; 5F3A81F3FC42914F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.4%; Score 105; DB 2;
85.7%; Pred. No. 8.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.4%; Score 105; DB 2; 90.5%; Pred. No. 8e-09; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
                                  STRAIN=BNC1;
MEDLINE-21091958; PubMed-11157232;
                                                                                                                                                                                                                                        STRAIN-BNC1;
MEDLINE-21091959; PubMed-11157233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00301; EFACTOR_GTP; 1. GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 AA; 42794 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KGKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KAKFERTKPHVNIGTIGHIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELONGATION FACTOR TU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
     SEQUENCE FROM N.A.
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-TU1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 19
09RG53
AC 09RG53,AC 09RG53,AC 09RG53,AC 09RG53,AC 00 AG 01-MAY.
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9RG53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RG53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M., Complete genome sequence of a virulent isolate of Streptococcus
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
  Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004166; GTP_EFTU_D2.
InterPro; IPR004166; GTP_EFTU_D3.
Pfam; PF001099; GTP_EFTU_D3. 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGANRFCT.
PROSITE; PS00301; EFGCTOR_GTP; 1.
ELONGATE; PR00515; COMPLETE PROTECOME.
SEQUENCE 398 AA; 43970 MW; 5CB2F8F5FA5101A0 CRC64;
                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DC-2001 (TrEMBLrel. 19, Last annotation update)
TRANSLATION ELONGATION FACTOR FU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
Score 106; DB 16;
Pred. No. 5.6e-09;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.2%; Score 106; DB 16;
85.7%; Pred. No. 5.6e-09;
                                                                                                                                                                                                                                                                                      398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDTA-degrading bacterium BNC1.
Bacteria; Proteobacteria; alpha subdivision.
NCBI_TaxID=85561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=TIGR4;
MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Э;
,
                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
  86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 293:498-506(2001).
EMBL; AE007444; AAK75581.1;
TIGR; SP1489; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                                   3 KEKYDRSKPHVNIGTIGHVDH
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 18; Conserv
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F9S8;
01-MAR-2001
                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
     Query Match
                             Best Local
Matches 1
```

ö

Q9F9S8

Ξ

18

RESULT Q9F9S8

ò g

401 AA; 43574 MW; B8ED827C1A717BA0 CRC64;

SEQUENCE

```
δ
                                                                                                                                                                Op
                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAILS-SERONAR LAI:
MEDLINE-94014964; PubMed-8409911;
Gravekamp C., Van de Kemp H., Franzen M., Carrington D., Schoone G.J.,
Van Eys G.J., Everard C.O., Hartskeerl R.A., Terpstra W.J.;
"Detection of seven species of pathogenic leptospires by PCR using two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                           Streptomyces aureofaciens.
Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                            Kormanec J., Nguyen L.D., Novotna J., Knirschova R., Weiser J.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL: AF368284; AAK54131.1; SEQUENCE 397 AA; 43683 MW; BF107EA8036FEF82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SEROVAR LAI;
MEDLINE-2008883; PubMed-10620683;
Sucrner R.L., Harskeer R.A., van de Kemp H., Bal A.E.;
"Characterization of the Leptospira interrogans S10-spc-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leptospira interrogans.
Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 105; DB 2; Lv 85.7%; Pred. No. 8.2e-09; iive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 AA
                                              397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Operon.";
FEMS Microbiol. Lett. 182:303-308(2000).
EMBL: AF115283; AAD40614.1;
HASSP, P02390; IEFU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D3; I.
Pfam; PR03145; GTP_EFTU_D3; I.
PRMYS; PR0315; ELONGATNFCT.
R PROSITE, PS00301; EFACTOR_GTP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cs of primers.";
Gen. Microbiol. 139:1691-1700(1993).
                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KAKFERTKPHVNIGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XD38;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-DEC-2001 (TrEMBLrel. 19,
ELONGATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.77
Matches 18; Conservative
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                             ELONGATION FACTOR TU
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sets of primers."
                                                                                                                                                                                                                                                                               NCBI_TaxID=1894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                      STRAIN-84/25;
                                                                 Q93T39;
                                           Q93T39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09XD38
RESULT 20
                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOCOS ON THE STANT OF THE STA
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NINE MILE PHASE I;
MEDLINE-20002589; PubMed=10531263;
MEDLINE-20002589; PubMed=10531263;
Sabhadri R., Hendrix L.R., Samuel J.E.;
"Differential expression of translational elements by life cycle variants of Coxiella burnetii.";
Infect. Immun. 67:6026-6033(1999).
EMBL; AF136604; AAD32649.1; -.
HSSP; P02990; IEFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE ELONGATION FACTOR TU PROTEIN.
Rhizoblum melliloti (Sinorhizoblum melliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizoblum.
                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
Score 105; DB 2; Length 401;
Pred. No. 8.3e-09;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.9%; Score 102; DB 2; Length 358;
85.7%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
39448 MW; 4355D7A33B0CCF2C CRC64;
                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04161; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03143; GTP_EFTU_D3; 1.
PROM15; PR00315; ELONGATNFCT.
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN-1021;
MEDLINE-21368234; Pubmed-11474104;
                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                     3 KEKFDRSKPHLNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KEKFVREKPHVNVGTIGHVDH 23
     85.4%;
81.0%;
                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, EF-TU (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7<sup>3</sup>
Matches 18; Conservative
                       Best Local Similarity 81.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Coxiella group; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q925Y6
                                                                                                                                                                         RESULT 22
Q9x6G1
                                                                                                                                                                                                                09x6G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
Q925Y6
```

σ

```
Moraxella sp. TACII25.
Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.
NCBI_TaxID=103760;
                                                                                                                                                                                                                                                         STRAIN=TAC II 25, MEDDMED=11112539; MEDLINE=20563866; PubMed=11112539; Masullo M., Arcari P., de Paola B., Parmeggiani A., Bocchini V.; Psychrophilic elongation factor Tu from the antarctic Moraxella sp. Tac II 25: biochemical characterization and cloning of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AD149258; CAB65285.2; -. P02390; IEFU. INTER. INTERVO. IEFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 AA; 43171 MW; 6A1217B78105A1B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) ELONGATION FACTOR TU.
                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.3%; Score 100; DB 2; Le
81.0%; Pred. No. 5.3e-08;
ive 1; Mismatches 3;
                                         393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21235186; PubMed=11337471;
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 39:15531-15539(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRIMTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 81.3
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                           PRELIMINARY;
                                                                                                                               ELONGATION FACTOR TU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=IL1403;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=TAC II 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                             Arcari P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                          Q9RAJ9;
                                           Q9RAJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CEIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26
                                                                                                                                                                                                                                                                                                                                                      gene.
       RESULT
                        Q9RAJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CEIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                             Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
Barloy-Hubler F., Barnett M.J., Becker A., Bolstard P., Bothe G.,
Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Rahn D.,
Rahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
Rahn D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
Ransperger U., Surzycki R., Thebault P., Wandenbol M.,
Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
Science 293:668-672(2001).
REMBL, ALS91787; CAC45933.1;
REMBL, ALS91787; CAC45918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and characterization of the chloroplast elongation factor EF-
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. JAPONICA NIPPONBARE;
MEDILINE=20062172; PubMed=10597036;
Lee J.H., Lee J.W., Chung Y.Y., Paek K.H., Shin J.S., Yun C.H.,
Kim J.K.;
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%; Score 102; DB 10; Length 467; 94.7%; Pred. No. 3e-08; 1.1ve 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                             Score 102; DB 16; Length 391;
Pred. No. 2.5e-08;
); Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00316; ELOMGATNECT.
PROSITE; PS00301; ERACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 467 AA; 50354 MW; 79A119279A7F1847 CRC64;
                                                                                                                                                                                                                                                                            391 AA; 42749 MW; 8846A34F44753693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST TRANSLATIONAL ELONGATION FACTOR TU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                 ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tu CDNA of Oryza sativa L.";
MO1. Cells 9:484-490(1999).
EMBL; AF145053; AAF15312.1; -.
HSSP; P07157; IAIP.
                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                          3 KSKFERNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                               82.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 KFERTKPHVNIGTIGHVDH 81
                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                           Query Match 82.9
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9SEFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SEF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 24
```

Q9SEF8

õ g qq

õ

ö

Gaps

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09TJ08;
      DDR READ DR RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast.
Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY EF-TU/EF-1A SUBFAMILY. EMBL; AF022186; AAF12934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20496959; PubMed-11040290;
Glockner G., Rosenthal A., Valentin K.;
"The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF.
                                                                                                                                                                                 ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Mol. Evol. 51:382-390(2000).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                 Query Match 80.5%; Score 99; DB 16; Length 395; Best Local Similarity 81.0%; Pred. No. 7.7e-08; Matches 17; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO'S IDENO(0795); GTP_EFTU.
INTERPRO'S IPRO(04161; GTP_EFTU_D2.
INTERPRO'S IPRO(04161; GTP_EFTU_D2.
INTERPRO'S IPRO(04160; GTP_EFTU_D3.
PÉTAM; PF001009; GTP_EFTU_D2; 1.
PÉTAM; PF03144; GTP_EFTU_D2; 1.
PRIMIS, PR00315; ELONGATHERY.
PROSITE; PS00301; EFRACTOR_GTP; 1.
Chloroplast; Elongation factor; GTP-binding; Hypothetical |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.7%; Score 98; DB 8; Length 410; 76.2%; Pred. No. 1.2e-07; Live 3; Mismatches 2; Indels
                                                                 C8D138A5147213F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 AA; 44731 MW; 66862440F7D54B65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOSYNTHESIS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 44.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created),01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                             410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 AA
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
InterPro; IPR000795; GTP_EFTU. PRINTS; PR0315; ELONGATNFCT. Complete proteome; GTP-binding. SEQUENCE 395 AA, 43212 WW.
                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                3 KEVYDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RAKFERSKPHINIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanidium caldarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Q9TLV8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99W61
                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99W61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              099W61
    S K B B
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                             à
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE S. aureus (strain N315), and S.aureus (strain Mu50);

WEDLINE-21311952; PubMed-11418146;

A Kuroda M., Ohta T., UGhiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

A Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

A Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

A Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

A Kanehisa M., Hayashi H., Hiramatsu K.;

Whole genome sequencing of meticillin-resistant Staphylococcus

Tureus.";

Lancet 357:1225-1240(2001).

EMBL; AP003130; Bab41737.1;

EMBL; AP003130; Bab41737.1;

InterPro; IPRO00795; GTP_EFTU.

PROSITE; PS00301; EFACTOR_GTP. I.

PROBLECE 394 AA; 43103 MW; A107A786B452C03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Prototheca.
NCBL_TaxID=3111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=263-11;
Knauf U., Hachtel W.;
A 22 kb fragment of the 53 kb plastid genome of the colourless alga
Prototheka wickerhamii containing atp-, rpl-,rps-, rrn-, and trn-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes.";
submitted (AUG-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
BIOSYNTHESIS (BY SIMILARITY).
-!- SUBCELULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONG TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EMBL; AJA45645; CAB53113.1; -.
HSSP; P07157; lAIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.9%; Score 97; DB 16; Length 394; 81.0%; Pred. No. 1.6e-07; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROTEIN SYNTHESIS ELONGATION FACTOR TU.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) TRANSLATIONAL ELONGATION FACTOR TU.
                                                    TUFA OR SA0506 OR SAV0548.
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain M150).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBL_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KEKFDRSKEHANIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prototheca wickerhamii.
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tu cDNA.
                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                           Q9AXU2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9AXU2
                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Q9AXU2
                                                                                                                                                                                                                                                                                                                                                                       g
   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
              Inter....
InterPro: IPR0041bu, .....
Pfam; PP00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRO315; PR00315; ELONATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Chloroplast; Blongation factor; GTP-binding; Protein blosynthesis.
"Fronience 409 AA; 44707 MW; D42945D21604A57B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana sylvestris (Wood tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                            Brandt P., Fartmann B., Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Created)
TrEMBLrel. 01, Last Sequence update)
(TrEMBLrel. 19, Last annotation update)
BLONGATION FACTOR TUR (EF-TUA) PRECURSOR (FRAGMENT).
                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 97; DB 3; Length 437; Pred. No. 1.8e-07; 0; Mismatches 1; Indels
                                                                                                                        Score 97; DB 8; Length 409;
Pred. No. 1.7e-07;
L; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B. Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             German Neurospora genome project;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513467; CAC28833.1; -.
HSSP, P02990; 1EFU.
                                                                                                                                                                                                                                            01-JUN-2001 (TremBirel. 17, Created)
01-JUN-2001 (TremBirel. 17, Last sequence update)
01-DEC-2001 (TremBirel. 19, Last annotation update)
PROBABLE TRANSLATION ELONGATION FACTOR EF-TU PRECURSOR, MITCCHONDRIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPRO00795; GTP_EFTU.
PRINTS; PR00315; ELONGATNRCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; GTP-binding; Protein biosynthesis.
SEQUENCE 437 AA; 47848 MW; 2F64E769FE7CEE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457 AA.
                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
          IPR004161; GTP_EFTU_D2. IPR004160; GTP_EFTU_D3.
                                                                                                                                                                               RAKFERKKPHVNIGTIGHVDH 23
InterPro; IPR000795; GTP_EFTU
                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
94.4%;
                                                                                                                          78.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 FNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 FORTKPHVNIGTIGHVDH 58
                                                                                                                          Query Match 78.9 Best Local Similarity 81.0 Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q40450
Q40450;
O1-NOV-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                           Q9C2P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                         RESULT 30
                                                                                                                                                                                        m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q40450
  õ
                                                                                                                                                                                       g
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OC OE DIT
```

```
Murayama Y., Matsubayashi T., Sugita M., Sugiura M.;
"Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu species.";
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00195; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004165; GTP_EFTU_D2.
InterPro; IPR004165; GTP_EFTU_D3.
Pfam; PF001009; GTP_EFTU; I.
Pfam; PF03144; GTP_EFTU_D3; 1.
PROSITE; PS03101; EFTU_D3; 1.
ELONGATION factor; GTP_Inding; Protein biosynthesis; Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINE-20550852; PubMed=11101151; Kang C.J., Lee M.G., Cho Y.S., Lee J.W., Kyung Y.J., Shin J.S., Kim E.S., Kim J.K., "Characterization of geranium (Pelargonium graveolens) chloroplast EF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pelargonium graveolens (rose geranium).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Geraniales; Geraniaceae; Pelargonium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLOROPLAST ELONGATION FACTOR TUA
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF00009; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNRCT.
PROSTITE; PS00301; EFACTOR_GTP; 1.
ELONGATION GACLOR; GTP-Pinding; Protein biosynthesis.
SEQUENCE 474 AA; 51315 MM; A321742468553865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49732 MW; 8A30C50DC137F755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST TRANSLATIONAL ELONGATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.0%; Score 96; DB 10; L
89.5%; Pred. No. 2.8e-07;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 22:767-774(1993).
EMBL; D11375; BAA01974.1; -.
HSSP; P02990; 1EFU.
                                                                                                                                              TISSUE=LEAF;
MEDLINE=93363910; PubMed=8358028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO1. Cells 10:579-583(2000).
EMBL; AF234537; AAK08141.1;
HSSP; P02990; IEFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 KFERKKPHVNIGTIGHVDH 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 89.5
hes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            >457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457 4
457 AA;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1
```

```
MEDLINE=93363910; PubMed=8358028;
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95TV3;
                                                                                                                                                                                                                                                                                                                                                                                                                       Q95TV3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709V6Q
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
Q95TV3
                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFTUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09V607
ID 09
AC 09
DT 01
  δλ
                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                         Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayshizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Mayers M.C., Miranda M., Narusska M., Nguyen M., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Suthwick A., "Full Length cDNA of gene AT4920360 (GI:7268831)."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94373864; PubMed=8087886;
Sugita M., Murayama Y., Sugiura M.;
"Structure and differential expression of two distinct genes encoding
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.0%; Score 96; DB 10; Length 476; 89.5%; Pred. No. 2.9e-07; live 0; Mismatches 2; Indels
             Length 474;
Score 96; DB 10; Length 4/2
Pred. No. 2.9e-07;
                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CHLOROPLAST TRANSLATION ELONGATION FACTOR EF-TU.
AT4G20360.
                                                                                                                                                                                                                                                                                                                                                                                                                                             476 AA; 51656 MW; 77B38DD1BB5386A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHLOROPLAST ELONGATION FACTOR TUB(EF-TUB) PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the chloroplast elongation factor Tu in tobacco."; Curr. Genet. 25:164-168(1994).
                                                                                                                                            476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 AA
                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana sylvestris (Wood tobacco)
                                                                                                                                            PRT;
                                 0
            78.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61-485 FROM N.A.
                                                         4 KFNRTKPHVNIGTIGHVDH 22
                                                                        4 KFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 KFERKKPHVNIGTIGHVDH 90
                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Elongation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=YOUNG LEAF;
                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUFA OR TUFB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       043364;
                                                                                                                                          093Y56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              043364
                                    Matches
                                                                                                                    RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    043364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                          δλ
                                                                                g
                                                                                                                                                    ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Murayama Y., Matsubayashi T., Sugita M., Sugiura M.; "Purification of chloroplast elongation factor Tu and cDNA analysis in tobacco: the existence of two chloroplast elongation factor Tu species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewisla S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY058403; AAL13722.1; -.
SEQUENCE 300 AA; 32987 MW; BECF21E546FBCDCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST ELONGATION FACTOR TUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.2%; Score 95; DB 5; Length 300; 76.2%; Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                               (EF-TUB).
FE88EF5D48B92D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GM14682P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 96; DB 10;
Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9V6Q7;
01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                  52688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 KFERKKPHVNIGTIGHVDH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity 89.5
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           485
                                                                                                                                                                                                                                                                                                                                                                                                485 AA;
```

119 AA

PRT;

PRELIMINARY;

```
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN BLOSYWTHESIS (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Chloroplast; Elongation factor; GTP-binding; Protein biosynthesis.
                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
                                                                                                                                                                                                                                                                                                                                                                                     Denny P., Preiser P., Williamson D., Wilson I.; "Evidence for a single origin of the 35 kb plastid DNA in
                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ELONGATION FACTOR TU (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y11429; CAA72237.1; -. HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexans.";
Protist 149:51-59(1998).
                                                                                                                                                                                                                          Theileria annulata.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5874;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-HISSAR
                                                                                                                                                                                                                                              Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                       078381;
                                                                                078381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 38
                                         RESULT
078381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09P909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                       RX Addans M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA dams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA dams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., 1 P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.
RA Brandon R.C., Banker E.G., Helt G., Nelson C.R., Miklos G.L.G.
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barcandale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barcandale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawley S., Volkiec C., Davenport L.B., Davies P.,
RA Borkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R. Borkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R. Borkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R. Durbin R.J., Evangelista C.C., Ferraz C., Ferriars S., Ploskomann W.,
RA Borkor D., Botcher A., Howland T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Weil M. H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Jalali M., Muthory D., Howland T.J., Weil M. H., Ibegwam C.,
RA Mount S.M., Moy M., Murphy B., Mizon R., Muzphy L., Muzny D.M., Nelson D.L.,
Ranckulov G., Milshim N.V., Mobarry C., Morris J., Moshrefi A.,
Rhount S.M., Moy M., Murphy B., Wenter E., Wang X.,
Reinert K., Remington K., Stungers R.D.C., Scheeler F., Shen H.,
Ryers R., Tector C., Turner R., Venter E., Wang X.,
Rang Z.-Y., Woodage T., Worley K.C., Wu D., Yeng S., Zho Q., Zhoo Q., Zhen R., Hogenon S., Wulliams S.M., Woodage T., Sungson M., Zhong G., Zhoo Q., Zhoo Q., Zhon R.,
Ryers R., Whyers E.W., Rubin G.M., Venter J.C.;
Rhenck R., Benner R., Worley E.W., Rubin G.M., Weissenbed. J.,
Rhenck R., Benner R., Worley E.W., Rubin G., Siden K., Benner R., Worley S., Wulliams S.M., Woodage T., Scheel
                                                                            Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 95; DB 5; Length 489;
Pred. No. 4.4e-07;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP-binding; Protein biosynthesis.
SEQUENCE 489 AA; 53992 MW; 9D09C36C4AEB2EE1 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00301; EFACTOR_GTP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000).
EMBL; AE003818; AAF58366.1; --
HSSP; P02990; 1ETU.
FlyBase; FBGn0024556; EfTuM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00315; ELONGAINFCT
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                              EFTUM OR CG6050.
                      01-DEC-2001 (T. CG6050 PROTEIN
```

119 AA; 13312 MW; 122F230BC0340BEC CRC64;

```
ó
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20365717; PubMed=10910347; Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alvas L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H. Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M. Coutinho L.L., Cristofani M., Dias Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                        ö
   Length 119;
Query Match 76.4%; Score 94; DB 8; Length 119
Best Local Similarity 71.4%; Pred. No. 1.3e-07;
Matches 15; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                         396 AA.
                                                                                                                                                                                                                                          01-071-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequ
01-DEC-2001 (TrEMBLrel. 19, Last anno
ELONGATION FACTOR TU.
XF2640 AND XF2628.
                                                                                                                                                                                                           PRT;
                                                                           22
                                                                                              3 KKQFLRNKPHINIGTIGHIDH
                                                                           2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-9A5C
                                                                                                                                                                                                                                                                                                                                                                             xylella
                                                                                                                                                                                                                              09P909;
                                                                                                                                                                                                           09P909
```

ö

Gaps

ö

2

16; Conservative

Query Match Best Local Similarity Matches 16; Conservat

77.2%; 76.2%;

2 KEKFNRTKPHVNIGTIGHVDH 22

ò q

```
ö
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Marino C.L.,

Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,

Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

Mardon D.H., Nagai M.A., Nassimento A.L., O.Ivveira M.A.,

Moon D.H., Nagai M.A., Nassimento A.L., Pesquero J.B.,

Moon D.H., Nagai M.A., Pereira R.C., Palmieri D.A., Paris A.,

Mardon M.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,

Margoto R.B., Poberto P.G., Rodrigues V., de Rosa M.J.M.,

de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,

A Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

A de Souza A.P., Terenzi M.F., Truffi D., Tsal S.M., Tsubako M.H.,

Nallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

A Sago M.A., Zatz M., Meidanis J., Setubal J.C.;

The genome sequence of the plant pathogen Xylella fastidiosa.";

Marture 406:151-159(2000).

C. Shullariy: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

BRBL; AE0040051 AAF86435.1;

InterPro; IPRO0315; ELONGATNECT.

PROSITE: PRO0315; ELONGATNECT.

PROSITE: PRO0315; ELONGATNECT.

PROMPIECE Proteomes GTP-binding.

WARDON SPOIRENER 306. AA. A. ARRA, MARANERA PARCEGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark M.A., Baumann L., Thao M.L., Moran N.A., Baumann P.;
"Degenerative Minimalism in the Genome of a Psyllid Endosymbiont.";
J. Bacteriol. 183:1853-1861(2001).
Bacteriol. 183:1853-1861(2001).
HSSP: P07157; IAIP.
InterPro: IPR000795; GTP_EFTU_D2.
InterPro: IPR004161; GTP_EFTU_D2.
InterPro: IPR03444; GTP_EFTU_D2: IPR03444; GTP_EFTU_D3: IPR03444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Candidatus Carsonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.4%; Score 94; DB 16; Length 396; 76.2%; Pred. No. 5e-07; 1ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42876 MW; 894CD061AE92E2E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44056 MW; 2524B4E2BD62E062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FINGRATION FACTOR TU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21125546; PubMed=11222582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QDKFKRTKLHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candidatus Carsonella ruddii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 76.4
Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=114186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09AIG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
Q9AIG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99AIG6
                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                 Toxoplasma gondii.
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
Toxoplasma.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                    Denny P.W., Wilson R.J.M.;
"An elongation factor encoded by the toxoplasma gondii putative
plastid.";
                            ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 401;
  Length 398;
76.4%; Score 94; DB 2; Length 398
76.2%; Pred. No. 5.1e-07;
.ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 94; DB 5; Length 401
76.2%; Pred. No. 5.1e-07;
Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation factor; GTP-binding; Protein biosynthesis. SEQUENCE 401 Aa; 44294 MW; C7C8B9F3ACF7530F CRC64;
                                                                                                                                                                                            Last sequence update)
Last annotation update)
TU.
                                                                                                                                                     401 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 22, 2002, 07:45:22 Job time: 141 sec
                                                                                                                                                                                Created)
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D2; 1.
                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                    3 KKKFNREKIHLNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X88775; CAA61254.1; -.
HSSP; P02990; 1EFU.
                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, PREDICTED ELONGATION FACTOR
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                 Similarity
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=5811;
                              16;
                                                                                                                                                                                                                                                                                                                                  STRAIN-RH;
    Query Match
                 Best Local
                                                                                                                                                   Q26114
Q26114;
                                                                                                                          40
                                                                                                                          RESULT
Q26114
                                                                                 qq
                                                                                                                                                                  Dp
                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
```

```
probable translatice congation factor translation elonga translation elonga
                                                                                                                                                                     translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
translation elonga
elongation factor
translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation elonga
translation elonga
probable translati
translation elonga
                                                      elongation factor
translation elonga
translation elonga
elongation factor
elongation factor
translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elonga
elonga
                protein translatio
translation elonga
translation elonga
                                                                                                                                            elonga
elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation elonga
translation elonga
probable translati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation e
translation e
translation e
                                                                                                                                            translation
translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302240
336183
521567
560659
536184
JC1420
JH0416
S75862
G72243
AH3344
C71672
S62726
H97825
A44795
S31151
G87143
                                                                                                                                                                                                                                          EFEGT
S73503
D60663
E71844
C84991
B70300
G70465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E86857
A54536
E75533
                                                                                                                                                                     EFYMTS
S23908
S23909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D26956
C60663
S73208
S04391
F69822
F69822
F7144381
S00229
S17146
S29293
S09153
S09153
                                                                                                                F83111
F60663
D95173
F98039
                                                                                                                                                                                                                S50138
PC4060
                                                                                                                                                                                                                                                                                                                                                                                               D97594
AB2816
                                                                                                                                                                                                                                                                                                                                                                                                                           AC2818
JC5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                       I40216
C70159
S62725
S23851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G71528
B86500
F72123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   981685
                                                                                                                                                                                                                                                                                                                                                                                  C97596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \overline{\mathbf{v}} \overline{\mathbf{
  translation elonga
translation elonga
protein chain elon
protein chain elon
translation elonga
translation elonga
hypothetical prote
elongation factor
protein chain elon
elongation factor
protein chain elon
elongation factor
translation factor
translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elonga
elonga
elonga
elonga
                                                                                               Search time 26.88 Seconds (without alignments) 78.645 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation elonga
protein translatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation elonga
elongation Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation elonga
translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rranslation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation elonga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation e
translation e
translation e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rranslation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                      283138
                 4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                      Minimum Match 08
Maximum Match 1008
Listing first 100 summaries
                                                                       - protein search, using sw model
                                                                                                   07:43:02
                                                                                                                                                                                     1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E64670
B90663
B90663
BFECT
EFECTA
S13561
S13560
E64078
F91152
G91241
D82332
G82337
AB06089
AB0457
AE0025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB5998
AD0934
AD1005
AD1406
AD1782
S78248
A81392
AE3346
S78139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T10168
                                                                                                                                                                                                                                                                                                                seq length: 0 seq length: 2000000000
                                                                                                  August 22, 2002,
                                                                                                                                                         US-09-488-737-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                           pir1:*
pir2:*
pir3:*
                                                                                                                                                                                                                                                                                                                                                                                                              PIR_71:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . . . . .
                                                                                                                                                                                                                                                                                                                                                         Post-processing:
                                                                                                                                                                                                                                                                                      Total number of
                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB :
Maximum DB :
                                                                         OM protein
                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                     ü
O
```

```
elongation Factor Tu (Ef-Tu) [imported] - Clostridium acetobutylicum
C; Species: Clostridium acetobutylicum
C; Species: Clostridium acetobutylicum
C; Date: H-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Accession: H97285
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; L.
J; Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium
A; Reference number: A96500; MUID:21359325; PMID:21359325
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 ckUR>
A; Residues: 1-397 ckUR>
A; Residues: 1-397 ckUR>
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; A; Genetics:
A; A; Genetics:
A; A; Genetics:
A; A; A; A; A; A; A; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation elongation factor EF-Tu.B [validated] - Escherichia coli

N;Contains: GTPase (EC 3.6.1.)

N;Contains: GTPase (EC 3.6.1.)

C;Species: Escherichia coli

C;Species: Bscherichia coli

C;Accession: A91478; A91095; A92332; I58035; G65204; A03518; A91475

R;An, G; Friesen, J.D.

Gene 12, 33-39, 1980

A;Title: The nucleotide sequence of tufB and four nearby tRNA structural genes of Esc
A;Reference number: A91478; MUD:8116558

A;Reference number: A91478; MUD:8147968; PIDN:AAA24669.1; PID:g147969

A;Residues: 1-394 <ANG>
A;Coss-references: GB:J01717; NID:g147968; PIDN:AAA24669.1; PID:g147969

B;Jones, M.D.; Petersen, T.E.; Nielsen, K.M.; Magnusson, S.; Sottrup-Jensen, L.; Gaus
Bur. J. Biochem. 108, 507-526, 1980

A;Reference number: A91095; MUD:81003875

A;Recession: A91095

A;Accession: A91095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-13 <RES.
A;Residues: 1-13 <RES.
B;Bustus: P. R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 112; DB 2; Length 39
Pred. No. 2.6e-09;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 2-394 < LAU>
R; Hudson, L; Rossi, J; Landy, A.
N; Hutre 294, 422-427, 1981
A; Title: Dual function transcripts specifying tRNA and mRNA.
A; Reference number: IS8035; MUD:82080657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KEKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation elongation factor EF-Tu Bacteroides fragilis, C;Species: Bacteroides fragilis
C;Accession: B60663
R;Ludwig, W.; Weizenegger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenho, Microbiol. 153, 241-247, 1990
A;Title: Complete nucleotide sequences of seven eubacterial genes coding for the elongat A;Reference number: A60663; MUID:90240875
A;Reference number: B60663
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-394 <LUD>
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homology cETU>
C;Superfamily: translation elongation factor Tu homology cETU>
C;Superfamily: translation elongation factor Tu homology cETU>
F;136-139/Region: GTP-binding NKXD motif
F;136-139,Region: GTP-binding SAK/L motif
F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: E64670
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Natures 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCOSS-references: GB:AE000626; GB:AE000511; NID:q2314360; PIDN:AAD08250.1; PID:q231436 (CSUperfamily: translation elongation factor Tu; translation elongation factor Tu homolo (CSE) and the constant of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                        C; Species: Helicobacter pylori
C; Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                          Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 118; DB 2; I
Pred. No. 3.2e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 112; DB 2; L
Pred. No. 2.6e-09;
0; Mismatches 1;
                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.27,
100.08; Pr.
                                                                                                                                                                                                                                                                                                     ranslation elongation factor EF-Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KEKFNRTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.1%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
Residues: 1-399 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
```

~

~

g ò

RESULT H97285

Matches

ò g

Thu Aug

```
A Hap position: 74 min
A Start codon: GTG
C;Function:
C;Function:
C;Function:
C;Function:
C;Function:
C;Function:
C;Function:
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu; or translation elongation factor Tu; translation elongation factor Tu; translation elongation factor Tu; translation elongation factor Tu;
C;Keywords: acetylated amino end; GTP binding; hydrolase; methylated amino acid; nucl;
C;Keywords: acetylated amino end; GTP binding; hydrolase; methylated amino acid; nucl;
C;S-26/Region: translation elongation factor Tu homology <FTU>
C;13-139/Region: cranslation elongation factor Tu homology <FTU>
C;13-139/Region: GTP-binding motif A (P-loop)
C;13-139/Region: GTP-binding SAK/L motif
C;Z-20/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
C;Z-26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #
C;S/Modified site: N6-methyllysine or N6,N6-dimethyllysine (Lys) (partial) #status e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: DNA
A; Residues: 1-394 <BLAT>
A; Residues: 1-394 <BLAT>
A; Cassar = Cassar 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Salmonella typhimurium
C; Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001
C; Accession: $13561
R; Tuboh, T.W.F.; Thompson, S.; Gesteland, R.F.; Hughes, D.; Atkins, J.F.
Biochim. Biophys. Acta 1050, 274-278, 1990
A; Title: The role of EF-Tu and other translation components in determining translocat A; Reference number: $13560; MUID:91002658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Residue: 1-394 <-TUO>
A; Residues: 1-394 <-TUO>
A; Residues: 1-394 <-TUO>
A; Ross references: EMBL:X55117; NID:g47947; PIDN:CAA38913.1; PID:g47948
A; Cross references: EMBL:X55117; NID:g47947; PIDN:CAA38913.1; PID:g47948
A; Cross references: EMBL:X55117; NID:g47947; PIDN:CAA38913.1; PID:g47948
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu hom C; Reywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis
F; 13-139/Domain: translation elongation factor Tu homology <-ETU>
                                                                                     A; Molecule type: protein
A; Residues: 60.264 < NNRX>
A; Nesidues: 60.264 < NNRX>
A; Note: this portion of the molecule was designated fragment B
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Recession: F65127
A; Accession: F65127
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S13561
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation elongation factor EF-Tu.B -{Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.2%; Score 111; DB 1; 90.5%; Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
A; Reference number: A61304; MUID:82189911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                        A; Accession: A61304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: tufA; strD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S13561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                              A; Molecule type: DNA
A; Residues: 1-394 < BLAP
A; Residues: 1-394 < BLAP
A; Residues: 1-394 < BLAP
A; Cross-references: GB-NEO00472; GB:U00096; NID:92367333; PIDN:AAC76954.1; PID:91790412;
A; Experimental source: strain K-12, substrain M01655
B; Kawashima, T.; Berthet-colominas, C.; Wulff, M.; Cusack, S.; Leberman, R.
Bubmitted to the Brookhaven Protein Data Bank, July 1996
A; Reference number: A65506; PDB:IEFU
A; Rontents: annotation; X-ray crystallography, 2.5 angstroms
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
B; Rawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
B; Rawashima, T.; Colominas, C.B.; Wulff, M.; Cusack, S.; Leberman, R.
A; Title: The structure of the Escherichia coli EP-Tu.EF-Ts complex at 2.5angstroms resol
A; Reference number: A58848; MUID:96170031
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Nakamura, S.; Nakayama, N.; Takahashi, K.; Kaziro, Y.
J. Biochem. 91, 1047-1063, 1982
A;Title: Primary structure of the polypeptide chain elongation factor Tu from Escherichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Jones, M.D.; Petersen, T.E.; Nielsen, K.M.; Magnusson, S.; Sottrup-Jensen, L.; Gausing Eur. J. Blochem. 108, 507-526, 1980
A.; Title: The complete amino-acid sequence of elongation factor Tu from Escherichia coli. A; Reference number: A91095; MUID:81003875
A; Accession: 891095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 2-394 <JONS
R;Laursen, R.A.; L'Italien, J.J.; Nagarkatti, S.; Miller, D.L.
J. Biol. Chem. 256, 8102-8109, 1981
A;Title: The amino acid sequence of elongation factor Tu of Escherichia coli. The comple
A;Reference number: A92332; MUID:81264196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation elongation factor EF-Tu.A [validated] - Escherichia coli
N;Contains: GTPase (EC 3.6.1.-)
C;Species: Escherichia coli
C;Date: 30-Nov-1980 #sequence_revision 09-Jun-1994 #text_change 19-Jan-2001
C;Accession: A91475; B91095; B92332; A61304; F65127; A03518; A91478
R;Yokota, T.; Sugisaki, H.; Takanami, M.; Kaziro, Y.
Gene 12, 25-31, 1980
A;Title: The nucleotide sequence of the cloned tufA gene of Escherichia coli.
A;Reference number: A91475; MUID:81165557
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 111; DB 1; Length 394; 90.5%; Pred. No. 3.7e-09; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-394 <YOK>
A;Cross-references: GB:J01690; NID:g147889; PID:g147897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 2-394 < LAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: tufB
A;Map position: 90 min
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B92332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

4

```
protein chain elongation factor EF-Tu [imported] - Escherichia coli (strain 0157:H7, C.Species: Escherichia coli (c.Species: Escherichia coli (c.Species: Bs-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C.Accession: G91241 R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. gasawatra, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: G91241 A;Status: preliminary A;Residues: 1-394 <AAx>
A;References: GB:BA000007; PIDN:BAB38326.1; PID:g13364379; GSPDB:GN00154 A;Cross-references: GB:BA000007; PIDN:BAB38326.1; PID:g13364379; GSPDB:GN00154 A;Cross-references: GB:BA000007; PIDN:BAB38326.1; PID:g13364379; GSPDB:GN00154 A;Genetics: ECS4903
C;Genetics: ECS4903
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                Alote: two copies of this gene are found in the Haemophilus influenzae chromosome C; Superfamily: translation elongation factor Tu; translation elongation factor Tu c. Keywords: GTP binding; nucleotide binding; P-loop; protein biosynthesis F;13-139/Domain: translation elongation factor Tu homology <ETU> F;19-26/Region: mucleotide-binding motif A (P-loop) F;13-139/Region: GTP-binding NKXD motif F;174-176/Region: GTP-binding SAK/L motif F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein chain elongation factor EF-Tu [imported] - Escherichia coli (strain 0157:H7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: translation elongation factor Tu; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Hayashi, T.; Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res, 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7
A; Reference number: A99629; MuID:21156231; PMID:11258796
A; Recession: F91152
A; Status: presliminary
A; Molecule type: DNA
A; Residues: 1-394 < HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000007; PIDN:BAB37613.1; PID:g13363663; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 111; DB 2; L 90.5%; Pred. No. 3.7e-09; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 111; DB 2; L. Larity 90.5%; Pred. No. 3.7e-09; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: F91152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: ECs4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     쉼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Gene: tufA

C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold

C; Superfamily: translation elongation factor Tu homology cETU>

F; 13-13-19/Domain: translation elongation factor Tu homology cETU>

F; 13-13-19/Region: ucleotide-binding motif A (P-loop)

F; 136-139/Region: GTP-binding NKXD motif

F; 136-136/Region: GTP-binding SKK/L motif

F; 174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation elongation factor EF-Tu.A - Salmonella typhimurium
C.Species: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001
C.Accession: S1356
B.Tuohy, T.M.F.; Thompson, S.; Gesteland, R.F.; Hughes, D.; Atkins, J.F.
Blochim: Bloophys: Acta 1050, 274-278, 1990
A.Title: The role of EF-Tu and other translation components in determining translocation
A.Reference number: S13560
A.Accession: S1356
A.Accession: S1356
A.Status: nucleic acid sequence not shown; translation not shown
A.Residues: DA
A.Residues: 1-394 <TUO>
A.Residues: 1-394 <TUO>
A.Residues: 1-394 <TUO>
A.Residues: Insulation to the EMBL Data Library, November 1990
C.Genetics:
                                                                                                               #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation elongation factor EF-Tu - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Accession: E64078; A64083
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, P, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Nelegenome random sequencing and assembly of Haemophilus influenzae Rd. A; Recession: E64078
B; Ratters nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
cA;Residues: 1-394 <TIG2>
A;Cross'references: GB:U32746; GB:L42023; NID:g1573626; PIDN:AAC22292.1; PID:g1573634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:L42023; NID:g1573559; PIDN:AAC22236.1; PID:g1573560;
                                                                                                               Ser)
                                                                                                            Asp,
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                               Lys,
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
F:19-26/Region: nucleotide-binding motif A (P-loop)
F:136-139/Region: GTP-binding NKXD motif
F:174-176/Region: GTP-binding SAK/L motif
F:25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Thr, Asn,
                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 394;
                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111; DB 2;
Pred. No. 3.7e-09;
1; Mismatches 1;
                                                                                                                                                                                                             Score 111; DB 2;
Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                       3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
                                                                                                                                                                                                      90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-394 <TIG1>
A; Cross-references: GB:U32739;
A; Accession: A64083
                                                                                                                                                                                                      Query Match 90.29
Best Local Similarity 90.59
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
```

U

ö

Gaps

ö

Indels

Length 394;

Б

and

hom

ô

Gaps

ó

Indels

Length 394;

U

ы

hom

G

UMGP:

ö

Gaps

ö

ö

Gaps

```
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AE0025
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Yersinia pestis
C;Date. 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0457
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Accession: A.M.: Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Davies, G. M. Butherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL590842; PIDN:CAC93222.1; PID:g15981670; GSPDB:GN00175 C;Genetics: A;Gene: tufA C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: tufB
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                         hypothetical protein tufB [imported] - Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005174; NID:g12518902; PIDN:AAG59176.1; GSPDB:GN00145; A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics:
                                                                                                                                                                                C;Accession: D86089
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, I iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, I Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
                                                                                                                                       C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elongation factor Tu [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%; Score 111; DB 2;
90.5%; Pred. No. 3.7e-09;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111; DB 2;
Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: VC0321
A;Map position: 1
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 1
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE004124; GB:AE003852; NID:99654770; PIDN:AAF93535.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE003852; NID:99654727; PIDN:AAF93494.1; GSPDB:GN001
O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation elongation factor EF-Tu VC0321 [imported] - Vibrio cholerae (strain N16961 C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C; Accession: G8237
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                          translation elongation factor EF-Tu VC0362 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: D82332
                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
  Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 111; DB 2; Length 39
Pred. No. 3.7e-09;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
Score 111; DB 2;
Pred. No. 3.7e-09;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111; DB 2;
Pred. No. 3.7e-09;
1; Mismatches 1.
                                                                                                                                          3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH 22
90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.2%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA

Kesidues: 1-394 < HEL>

A; Cross-references: GB: AE004120;

A; Experimental source: serogroup
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-394 <HEI>
                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: D82332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: G82337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: VC0362
  Query Match
                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

hom

```
Cibecies: Listeria monocytogenes
Cibecies: Disteria Disteria Disteria Disteria, Disteria, Disteria, Disteria Disteria, Disteria D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Salmonella enterica subsp. enterica subsp. enterica serovar Typhi (Cispecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (Species: Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 (Spacession: AD1005 (Spacession: AD00502; PMID:11677608 (AD1005 (Spacession: AD1005) (AD1005 (Spacession: AD1005) (AD1005 (Spacession: AD1005) (AD1005 (AD1005) (AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation elongation factor EF-Tu homolog tufA [imported] - Listeria monocytogenes
                                                C; Superfamily: translation elongation factor Tu; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: tufA
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL513382; PIDN:CAD08168.1; PID:g16505144; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                  Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.2%; Score 111; DB 2; Length 39
Best Local Similarity 90.5%; Pred. No. 3.7e-09;
Matches 19; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                  Score 111; DB 2; L
Pred. No. 3.7e-09;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109; DB 2;
Pred. No. 7.4e-09;
                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                  Query Match 90.2%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.6%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KEKFERTKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: AD1005
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
    A; Gene: tufB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein chain elongation factor EF-Tu [imported] - Escherichia coli (strain 0157:H7, sub C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C; Accession: 85998
B; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A; Reference number: A88480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <STO>
A; Residues: 1-394 <STO>
A; Cross-references: GB:AE005174; NID:g12517957; PIDN:AAG58446.1; GSPDB:GN00145; UWGP:Z46
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: tufA
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: tufA
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: AD0934
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterica serovar Typhi (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-394 <PAR>
A; Residues: 1-394 <PAR>
C; Cenetics: CB:AL513382; PIDN:CAD09494.1; PID:g16504611; GSPDB:GN00176
                                      A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUD:21470413; PMID:11586360 A;Accession: AB00025 A;Status: preliminary A;Nebicule type: DNA A;Residues: 1-394 <RUR>
A;Coss.-references: GB:AL590842; PIDN:CAC89064.1; PID:915978304; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elongation factor Tu [imported] - Salmonella enterica subsp. enterica serov: C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111; DB 2; Length 394;
Pred. No. 3.7e-09;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 111; DB 2; Length 394;
Pred. No. 3.7e-09;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 90.2%;
Best Local Similarity 90.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.2%;
Best Local Similarity 90.5%;
Matches 19; Conservative
Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
```

hom

```
A;Gene: tuf; Cj0470
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
F;13-139/Domain: translation elongation factor Tu homology <ETU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Map position: I
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation elongation factor EF-Tu.A - Reclinomonas americana (ATCC 50394) mitochond N;Alternate names: translation elongation factor tufA
                                                                                                                                                                                                                         translation elongation factor EF-Tu Cj0470 [similarity] - Campylobacter jejuni (strai
                                                                                                                                                                                                                                                    C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
C; Accession: A81392
C; W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 403, 665-668, 2000
A; Reference number: A81250; MUID:20150912
A; Accession: A8139
A; Accession: A8139
A; Molecule type: DNA
A; Residues: 1-399 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL139075; GB:AL111168; NID:q6967817; PIDN:CAB75108.1; PID:q696
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: AE3346
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-391 <KUR>
A;Resicules: 1-391 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51936.1; PID:g17982694; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 399,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.0%; Score 107; DB 2; L 90.5%; Pred. No. 1.5e-08; cive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 108; DB 2;
Pred. No. 1.1e-08;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.8%; Score 108;
                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KEKFSRNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.5%;
                                        3 REKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KSKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.0
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: BMEI0755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           878139
                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
      ò
                                                                                                                                                                                                                                                                                                          C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C; Accession: AD1782
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Doninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AD1782
A; Molecule type: DNA
A; Residues: 1-395 AGLA>
A; Cross-references: GB:AL592022; PIDN:CAC98028.1; PID:g16415338; GSPDB:GN00178
A; Residues: 1-395 AGLA>
C; Genetics:
A; Constrained a source: Strain Clipil262
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation elongation factor EF-Tu - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
C;Species: chloroplast Odontella sinensis
C;Species: chloroplast Odontella sinensis
C;Species: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 02-Feb-2001
C;Accession: S78248
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
A;Reference number: S78248
A;Reference number: S78248
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Rolecule
                                                                                                                                                                                                                                                                                         translation elongation factor EF-Tu homolog tufA [imported] - Listeria innocua (strain
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.6%; Score 109; DB 2; L
90.5%; Pred. No. 7.4e-09;
iive 2; Mismatches 0;
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 109; DB 2;
90.5%; Pred. No. 7.7e-09;
iive 1; Mismatches 1;
   Mismatches
   ä
                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                  3 KEKFDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KEKFDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.55
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.5
Matches 19; Conservative
   Conservative
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
   Matches
                                                                   ò
                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

08:03:50

22

Thu Aug

ьбd

```
translation elongation factor Tu NMB0124 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: A81235; D82006; C82008
R;Pettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, R;Pettelin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Atthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Reference number: A81000; MuID:2017575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;CrET>
A;Cross-references: 1-34
A;Cross-references: GB:AbC002371; GB:AbC02098; NID:g7225337; PIDN:AAF40583.1; PID:g722
A;Experimental source: serogroup B, strain MC58
B;Parkhill, J; Achtman, M; James, K.D; Benley, S.D; Churcher, C.; Klee, S.R; Mo
Holroyd, S.; Jagels, K; Leather, S.; Moule, S.; Mungall, K.; Quall, M.A.; Rajandre
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Reference number: A81775; MUID:20222556
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <PAR>
A;Residues: 1-394 <PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83449.1; PID:g737
A;Experimental source: serogroup A, strain 22491
A;Accession: C82008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:AL157959; NID:97378778; PIDN:CAB83464.1; PID:9737
A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PID:9722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: NWB0139
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE002372; GB:AE002098; NID:g7225350; PIDN:AAF40598.1; A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: tufA2; NMA0149
C;Superfamily: translation elongation factor Tu; translation elon
F;13-139/Domain: translation elongation factor Tu homology <FTU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 2; Length 394;
Pred. No. 1.5e-08;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 2;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KEKFERSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: tufAl; NMB0124; NMA0134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-394 <PA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics: <PAR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <PAR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                        A. Variety: ATCC 50394
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C; Accession: 578139
C; Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C; Accession: 578139
R; Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank
Nature 387, 493-497, 1997
A; Title: An ancestral mitochondrial DNA resembling a cubacterial genome in miniature.
A; Reference number: 578127; MUD:97311393
A; Accession: 578139
A; Accession: 578139
A; Reference number: 578127; MUD:97311393
A; Reference number: 578127
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-394 cLAN>
A; Ross-references: EMBL:AF007261; NID:92258325; PIDN:AAD11872.1; PID:92258338
A; Experimental source: ATCC 50394
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Naisseria gonorthoeae
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Date: 02-Jun-2000
C:Date: 02-Jun-2000
C:Date: 02-Jun-2000
C:Date: 02-Jun-2000
C:Date: 03-Jun-2000
C:Dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation elongation factor Tu NMB0139 [imported] - Neisseria meningitidis (strain MC5 C;Species: Neisseria meningitidis & C;Species: Neisseria meningitidis & C;Date: ,31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: DB1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation elongation factor Tu - Neisseria gonorrhoeae
C;Species: Neisseria gonorrhoeae
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 107; DB 2; Le
ilarity 85.7%; Pred. No. 1.5e-08;
Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%; Score 107; DB 2; L larity 90.5%; Pred. No. 1.5e-08; Conservative 0; Mismatches 2;
                                                                                                 Species: mitochondrion Reclinomonas americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KEKFERTKPHCNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KEKFERSKPHVNVGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Hic

7 Matches

ð a RESULT

```
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUD:99287316
A;Recession: 672243
A;Molecule type: DNA
A;Residues: 1-400 <ARN>
A;Cross-references: GB:AE001799; GB:AE000512; NID:g4982067; PIDN:AAD36569.1; PID:g498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribelvecchio, V.G.: Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov Ribelvecchio, V.G.: Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
Aritle: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain MSB8
R; Bachleitner, M.; Ludwig, W.; Stetter, K.O.; Schleifer, K.H.
FEMS Microbiol. Lett. 57, 115-120, 1989
A; Title: Nucleotide sequence of the gene coding for the elongation factor Tu from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: I
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein translation elongation factor Tu (EF-Tu) [imported] - Brucella melitensis (st
                                                                                                                                                                                                                                C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Feb-2001
C;Accession: G72243; A48314 A48314, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gree: TMISO2
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu hon C; Superfamily: translation elongation factor Tu; translation blosynthesis
C; Keywords: GTP binding; nucleotide binding; P-loop; protein blosynthesis
F;13-139/Domain: translation elongation factor Tu homology <ETU>
F;13-139/Pomain: nucleotide-binding motif A (P-loop)
F;136-139/Region: GTP-binding NK/L motif
F;174-176/Region: GTP-binding SAK/L motif
F;25,26,62,136,137,139,174/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: AAL51923.1; PID: 917982679; GSPDB: GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-39,'V',41-400 <BAC>
A;Cross-references: GB:M27479; NID:g154836; PIDN:AAA27415.1; PID:g552037
C;Genetics:
                                                                                                                                                                                                        translation elongation factor EF-Tu – Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 107; DB 2; Length 40
85.7%; Pred. No. 1.5e-08;
iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KEKFVRTKPHVNVGTIGHIDH 23
      A, Residues: 1-406 <KUR>
A, Cross-references: GB:AE008917; F
A, Experimental source: strain 16M
C, Genetics:
A, Gene: BME10742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A48314
A; Accession: A48314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: AH3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: AH3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31
                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Wolecule type: DNA
A; Residues: 1-396 CBRE>
A; Cross-references: EMBL: X82820; NID:g609255; PIDN:CAA58029.1; PID:g609256
A; Cross-references: EMBL: X82820; NID:g609255; PIDN:CAA58029.1; PID:g609256
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homology CFTU>
F; 13-139/Domain: translation elongation factor Tu homology CFTU>
F; 19-26/Region: nucleotide-binding motif A (P-loop)
F; 136-139/Region: GTP-binding NKXD motif
F; 174-176/Region: GTP-binding SAK/L motif
F; 174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Caulobacter crescentus
Cispecies: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 18-Jul-2001
Ciscession: A87403; E87645
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haft, D.H.; Kolon
N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Bremaud, L.; Fremaux, C.; Laalami, S.; Cenatiempo, Y.
Nucleic Acids Res. 23, 1737-1743, 1995
A;Title: Genetic and molecular analysis of the tRNA-tufB operon of the myxobacterium Sti
A;Reference number: S55281; MUID:95303606
A;Accession: S55281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: CC1240; CC3199
;Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-396 <STO>
A;Cross-references: GB:AE005673; NID:913422569; PIDN:AAK23221.1; GSPDB:GN00148
A;Accession: E87645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE005673; NID: 913424877; PIDN: AAK25161.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                 translation elongation factor EF-Tu - Stigmatella aurantiaca
C;Species: Stigmatella aurantiaca
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 02-Feb-2001
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 2; Length 396;
Pred. No. 1.5e-08;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.0%; Score 107; DB 2; L 90.5%; Pred. No. 1.5e-08; Live 0; Mismatches 2;
      ï
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
   5
                                                                 22
                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%;
90.5%;
                                                                 KEKFNRTKPHVNIGTIGHVDH
                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KEKFERNKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S55281; S52237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-396 <ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
```

RESULT

ò

g

~

ŏ

턴

us-09-488-737-1.rpr

ö

```
translation elongation factor EF-Tu - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 31-Dec-1993 **sequence_revision 31-Dec-1993 *text_change 02-Feb-2001
C;Accession: A44795; H70639; S22152
R;Carlin, N.I.; Lofdahl, S.; Magnusson, M.
Infect. Immun. 60, 3136-3142, 1992
A;Title: Monoclonal antibodies specific for elongation factor Tu and complete nucleot A;Reference number: A44795; MUID:92347983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
A;Accession: H70639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: tuf
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:Z84395; GB:AL123456; NID:g3261698; PIDN:CAB06471.1; PID:g18061
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cispedies: Rickettsia conorii
Cispedies: Rickettsia conorii
Cispedies: Rickettsia conorii
Cispedies: Bace 2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
Ciscession: H97825
Riogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2094, 2001
A;Fitle: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE006914; PIDN: AAL03546.1; PID: 915620123; GSPDB: GN00173 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamlin, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-396 < CAR>
A; Residues: 1-396 < CAR>
A; Residues: 1-396 < CAR>
A; Cross-references: EMBL:X63539; NID:g44686; PIDN:CAA45102.1; PID:g581383
A; Note: sequence extracted from NCBI backbone (NCBIN:109731, NCBIE:109732)
R; Cole, S.T; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, I.; Connor, R.; Devies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                               ö
                           C; Keywords: GTP binding; nucleotide binding; P-loop
F;13-139/Domain: translattion elongation factor Tu homology <FTU>
F;19-26/Region: nucleotide-binding motif A (P-loop)
F;136-139/Region: GTP-binding NKXD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.2%; Score 106; DB 2; 1
90.5%; Pred. No. 2.1e-08;
tive 0; Mismatches 2;
                                                                                                                                                                                                      Score 106; DB 2;
Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                       3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                      86.2%;
90.5%;
                                                                                                                                                                                                                                                                  19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 90.5
ses 19; Conservative
                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: H97825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 19
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                               음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; General tuf; RP661
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold C; Superfamily: translation elongation factor Tu homold C; Keywords: GTP binding; nucleotide binding; P-loop F; 13-139/Domain: translation elongation factor Tu homology <ETU>F; 19-26/Region: nucleotide-binding motif A (P-loop)
F; 136-139/Region: GTP-binding NRXD motif F; 174-176/Region: GTP-binding SAK/L motif F; 174-176/Region: GTP-binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genetic code: SGC3
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-394 <anb
A; Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15101.1; PID:g386120
A; Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-394 <GLA>
A;Cross-references: GB:AE002151; GB:AF222894; NID:g6899524; PIDN:AAF30935.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: tuf; UU522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T.; Alsmark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: C71672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: EMBL:234275; NID:g498790; PIDN:CAA84029.1; PID:g498791
Riglass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A.Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation elongation factor tu (EF-tu) UU522 [similarity] - Ureaplasma urealyticum
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                 translation elongation factor EF-Tu (tuf) RP661 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Ureaplasma urealyticum
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 02-Feb-2001
C;Accession: S62726; F82879
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: C71672
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                    Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 394;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
87.0%; Score 107; DB 2; I
90.5%; Pred. No. 1.5e-08;
Micmatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106; DB 2;
Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, June 1994
A; Reference number: S62726
A; Accession: S62726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
,
                                                                                                                                                22
                                                                                                                                                                              18 KSKFERTKPHVNIGTIGHVDH 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.2%;
90.5%;
                                                                                                                                             KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEKFNRTKPHVNIGTIGHVDH
                        Query Match 87.0
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: The complete
A; Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: F82879
A; Status: preliminar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33
                                                                                                                                                ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m
                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

ö

٠. د

D.; Gordon I.; Holroyd,

```
objection factor EF-Tu [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R;Cole, S.T.; Eiglmeier, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Nuthors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Title: Massive gene decay in the leprosy bacillus
A;Title: Massive gene decay in the leprosy bacillus
A;Title: Massive gene decay in the leprosy bacillus
A;Accession: G87143
A;Molecule type: DNA
A;Residues: 1-396 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: tuf
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB:AE004091; NID:g9950489; PIDN:AAG07665.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE004842; GB:AE004091; NID:99950481; PIDN:AAG07653.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Cross-references: GB:AL450380; NID:913093557; PIDN:CAC30831.1; GSPDB:GN00147
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elongation factor Tu PA4277 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Nov-2000
C;Accession: F3111; C83111; C8311; C83111; C83111; C83111; C83111; C83111; C83111; C83111; C8311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106; DB 2; L/
Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.2%; Score 106; DB 2;
85.7%; Pred. No. 2.1e-08;
tive 1; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: F83111
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 < STOAD
A; Residues: 1-397 < STOAD
A; Experimental source: strain PAO1
A; Accession: C83112
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-397 < ST2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: tufB; PA4277; tufA; PA4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KEKFERNKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KAKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.2 Best Local Similarity 85.7 Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39
           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
F60663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Mycobacterium leprae
C.Species: 33115; S34954; JC2020
C.Accession: S3115; S34954; JC2020
R.Honore, N.; Bergh, S.; Chanteau, S.; Doucet-Populaire, F.; Eiglmeier, K.; Garnier, T.;
Reloner, N.; Sittisombut, N.; Wu-Hunter, S.; Cole, S.T.
Mol. Microbiol. 7, 207-214, 1993
A.; Title: Nuclectide sequence of the first cosmid from the Mycobacterium leprae genome pr
A. Reference number: S31143; MUID:93188701
A. Reference number: S31143; MUID:93188701
A. Status: nucleic acid sequence not shown; translation not shown
A. Molecule type: DNA
A. Residues: 1-396 <-HON>
A. Residues: 1-396 <-HON>
A. Residues: Lasting and Sequence was submitted to the EMBL Data Library, August 1992
R. Silbaq, F.; Bercovier, H.
Nucleic Acids Res. 21, 3327, 1993
A.; Title: Nuclectide sequence of Mycobacterium leprae elongation factor (EF-Tu) gene.
A. Reference number: S34954; MUID:93341950
A. Recession: S34954
A. Reference number: S44954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A) Accession: JC2262
A; Molecule type: DNA
A; Residues: 'V', Z-128, GVPYILVA', 137, 'NKSDAVDDEELLE', 151, 'V', 153-280, 'L', 282-348, 'G', 356
A; Residues: 'V', Z-128, GVPYILVA', 137, 'NKSDAVDDEELLE', 151, 'V', 153-280, 'L', 282-348, 'G', 356
A; Cross-references: DDBJ:D13869
C; Genetics:
A; Genetics:
A; Genetics:
C; Genetics:
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-128, GVPTILVALNKSDAVDDEELLELV', 153-280, 'L', 282-348, 'G', 350-396 <SIL>
A; Residues: 1-128, GVPTILVALNKSDAVDDEELLELV', 153-280, 'L', 282-348, 'G', 350-396 <SIL>
A; Cross-references: EMBL: L13276, NID:9293241; PIDN:AAA71969.1; PID:9293242
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1993
R: Dhandayuthapani, S.; Banu, M.J.; Kashiwabara, Y.
Biochem. 115, 664-669, 1994
A; Title: Cloning and sequence determination of the gene coding for the elongation factor
A; Reference number: JC2262; MUID:94375410
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homold C; Superfamily: translation elongation binding; P-loop; protein biosynthesis F;13-141/Domain: translation elongation factor Tu homology <ETU> F;13-141/Domain: urcleotide-binding motif A (P-loop) F;138-141/Region: grp-binding NKXD motif F;138-141/Region: GTP-binding SAK/L motif F;175-177/Region: GTP-binding sak/L motif F;25,26,64,138,139,141,175/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 106; DB 2; Length 39
Pred. No. 2.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation elongation factor EF-Tu - Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%; Score 106; DB 2; L
90.5%; Pred. No. 2.1e-08;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.2%;
ilarity 90.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

M.J.; K.; L

ö

Gaps

ö

2; Indels

Length 397;

P.; Hickey, A.; Larbig,

ö

Gaps

ö

Length 396; Indels

translation elongation factor EF-Tu - Streptococcus oralis

```
C; Species: Streptococcus oralis
C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 02-Feb-2001
C; Accession: F60663
R; Ludwyq, W.; Welzenegger, M.; Betzl, D.; Leidel, E.; Lenz, T.; Ludvigsen, A.; Moellenhc Arciession: F60663
A; Title: Complete nucleotide sequences of seven eubacterial genes coding for the elongat A; Reference number: A60663; MUID:90240875
A; Accession: F60663
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-398 <LUD>
C; Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo C; Superfamily: translation elongation factor Tu homology <ETU>
C; Superfamily: Translation elongation factor Tu homology <ETU>
F; 13-142/Domain: translation elongation factor Tu homology <ETU>
F; 13-142/Region: GTP-binding NRXD motif
F; 177-179/Region: GTP-binding SAK/L motif
F; 25, 26, 65, 139, 140, 142, 177/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C: Accession: D95173
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A: Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A. Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A: Reference number: A95000; MUD:21357209; PMID:11463916
A: Accession: D95173
A: Stell special and any A: Assidues: 1-398 ckUR>
A: Residues: 1-398 ckUR>
A: Residues: 1-398 ckUR>
A: Residues: 1-398 ckUR>
A: C: Genetics: Strain TIGR4
C: Genetics: Strain Tigra
C: Genetics: Strain Tigra
C: Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation elongation factor Tu [imported] - Streptococcus pneumoniae (strain TIGR4) C;Species: Streptococcus pneumoniae C;Date: 03-Aug_2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 86.2%; Score 106; DB 2; Length 398; Best Local Similarity 85.7%; Pred. No. 2.1e-08; Matches 18; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.2%; Score 106; DB 2; Length 398;
85.7%; Pred. No. 2.1e-08;
Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KEKYDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.29
Best Local Similarity 85.79
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

ö

Gaps

;

Search completed: August 22, 2002, 07:46:12 Job time: 190 sec

ò

Page

Appli Appli Appli Appli Appli Appli Appli Appli Appli

us-09-488-737-1.rai 08:03:49 2002

US-08-626-994A-3
US-08-626-994A-3
US-08-957-742-1
US-08-9626-944
US-08-9626-944
US-09-039-039-039-04
US-09-131-648-116
US-09-131-648-116
US-09-131-648-116
US-09-131-648-116
US-09-131-648-116
US-09-131-648-116
US-09-131-648-116
US-08-989-370-5
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-989-941B-3
US-08-999-375-526C-34
US-08-999-376-526C-34
US-08-999-376-526C-34
US-08-999-376-526C-34
US-08-999-378-6
US-08-999-3 498 519 865 887 915 915 1264 1264 1264 $\begin{array}{c} \mathbf{m} \\ \mathbf{$ 40.5 3, Appli 5, Appli 2, Appli 1, Appli 18, Appl Search time 21.52 Seconds (without alignments) 24.970 Million cell updates/sec Appli Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence 4, 1 Sequence 3, 2 Sequence 3, 2 Sequence 5, 2 Sequence 1, 3 Sequence 1, 3 Description Sequence Sequence Sequence Sequence Sequence Sequence Sednence
Sednence Patent No. /cgn2_6/ptcdata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PcTuS_COMB.pep:* 4.5 Compugen Ltd. US-09-174-768-4
US-08-454-439-19
US-08-454-109
US-08-45-19
US-08-45-19
US-08-45-1817-18
US-08-45-1817-18
US-08-45-439-18
US-08-221-817-20
US-08-45-439-20
US-08-45-439-20
US-08-45-439-20
US-08-45-439-20
US-08-65-699-40
US-09-655-699-40
US-09-655-538-40
US-09-565-538-40 US-09-140-466-6 US-09-140-466-4 US-09-140-466-3 US-09-140-466-5 US-09-140-466-5 US-08-399-351-1 US-08-371-377-18 5225348-1 hits satisfying chosen parameters: 231628 seqs, 24425594 residues ٠. SUMMARIES GenCore version Copyright (c) 1993 - 2000 Minimum Match 0% Maximum Match 100% Listing first 100 summaries sw model 2002, 07:43:01 US-09-488-737-1 123 1 MKEKFNRTKPHVNIGTIGHVDH 0.5 BLOSUM62 Gapop 10.0 , Gapext Issued_Patents_AA:* protein search, using length: 0 length: 2000000000 DB Length August 22, Query Match Post-processing: of

sed

0B DB

Minimum Maximum Database

Potal number

Searched:

Title: Perfect score:

Sequence:

ı

protein

ö

Run ŏ

Scoring table:

Appli Appli Appli , Appli , Appli , Appli , Appli 526827(

sequence 3, sequence 1, sequence 2, sequence 2, sequence 1, sequence 2, sequence 3, sequence 2, sequence 1, sequence 2, sequen

Appli , Appl

Appl

Appl

Appli Appli Appli Appli Appli Appli Appli

Appl Appl Appl Appl Appl

PCT-US92-08012-2 US-08-889-841B-44 US-07-772-032-2 US-09-157-077-9

PCT-US95-08565-12 US-09-442-100-11 US-09-106-075A-89 US-09-106-075A-90

Score

Result No.

, Appl Appli Appli

Appli Appli

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
Sequence 6, Application US/09140466

Fatent No. 6268160

GENERAL INFORMATION

APPLICANT: CLOUGH, BARBARA

APPLICANT: CLOUGH, BARBARA

APPLICANT: WILSON, ROBERT

TITLE OF INVENTION: AN EFTE TU PROTEIN ENCODED ON THE PLASTID DNA OF THE

TITLE OF INVENTION: AN EFTECTIVE AS ANTI-MALARIAL COMPOUNDS

TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS

FILE REPRESENCE: N66837B GCW PJC DP

CURRENT APPLICATION NUMBER: US/09/140,466

CURRENT FILING DATE: 1998-08-26

EARLIER FILING DATE: 1998-08-26

EARLIER PILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATENTIN VOS: 14

SOFTWARE: PATENTIN VOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09140466
Patent No. 6266160
GENERAL INFORMATION:
APPLICANT: PREISER
APPLICANT: PREISER
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: BFECTIVE AS ANTI-MALARIAL COMPOUNDS
TITLE OF INVENTION: BFECTIVE AS ANTI-MALARIAL COMPOUNDS
TITLE OF INVENTION: NUMBER: US/09/140,466
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT APPLICATION NUMBER: US/09/140,466
EARLIER PILING DATE: 1999-08-26
BARLIER PILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102; DB 4; Length 40
Pred. No. 1.1e-08;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111; DB 4;
Pred. No. 3.9e-10;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KEKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-140-466-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.9
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Cryptomonas phi
US-09-140-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-140-466-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
```

3 RDKFERSKPHVNIGTIGHVDH 23

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                          APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: PILISON, ROBERT
TITLE OF INVENTION: AN EF-TU PROFEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REFERENCE: NG8837B GGW PJC DP
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT FILING DATE: 1998-08-26
EARLIER PPLICATION NUMBER: US 60/056,246
EARLIER PPLICATION NUMBER: US 60/056,246
EARLIER PILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CLOUGH, BARBARA
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: PREISER, PETER
APPLICANT: WILSON, ROBERT
TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
TITLE OF INVENTION: MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
TITLE OF INVENTION: EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
FILE REPERENCE: N68837B GCW DJC DP
CURRENT APPLICATION NUMBER: US/09/140,466
CURRENT PILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: US 60/056,246
EARLIER FILING DATE: 1997-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.2%; Score 95; DB 4; Length 409; 76.2%; Pred. No. 1.5e-07; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.5%; Score 99; DB 4; Length 409
81.0%; Pred. No. 3.4e-08;
Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
; Sequence 3, Application US/09140466; Patent No. 6268160; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5, Application US/09140466; Patent No. 6268160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09140466
; Patent No. 6268160
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RAKFERTKPHANIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ROKFDGNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Cyanophora paradoxa
US-09-140-466-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Anacystis nidulans
US-09-140-466-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.5
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 76.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-140-466-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-09-140-466-2
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

```
APPLICANT: Fisher, Paul B.

APPLICANT: Shen, Ruoqian
TITLE OF INVENTION: DEPELOPMENT OF DNA PROBES AND
TITLE OF INVENTION: DEPELOPMENT OF DNA PROBES AND
TITLE OF INVENTION: MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 462,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                      ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 462 US-08-299-351-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,377
FILING DATE:
                                                                                                                                                                                                                                                          Score 51; DB 1;
Pred. No. 1.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 0575/37590-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 331-0525
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 2
Pred. No. 1.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 18, Application US/08371377; Patent No. 5851764; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
                                                                                                                                                                                                                                                          41.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.5%;
60.0%;
J. Biol. Chem.
264
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  7 RTKPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                    3 KEKTHINIVVIGHVD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | |:|| ||||||
3 KEKTHINIVVIGHVD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 RTKPHVNIGTIGHVD 21
                                                                              5791-5798
1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-371-377-18
                     JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: N
STATE:
                                                                                 PAGES:
                                                                                                             DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΩD
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSOR 239 -351-1
Sequence 1, Application US/0829351
Sequence 1, Application IS Sequence 1
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES:
ADDRESSE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1400 Mercantile Bank Tower, 1101 Walnut St.
CTUT: Kansas City
STATE: MISSOUTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                 TITLE OF INVENTION. MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS TITLE OF INVENTION AMLARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS TITLE OF INVENTIONS MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS TITLE OF INVENTIONS BY DO DO THE REFERENCE: NG8837B GGW DJC DP CURRENT APPLICATION NUMBER: US/09/140,466 CURRENT FILING DATE: 1998-08-26 EARLIER APPLICATION NUMBER: US 60/056,246 EARLIER PILING DATE: 1997-08-28 NUMBER OF SEC ID NOS: 14 SOFTWARE: PLANCE DATE: 1997-08-28 SOFTWARE: PREFERIT OF TO THE TOTAL OF THE TOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 78; DB 4; Length 410
Pred. No. 7.9e-05;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,351
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cleveland Jr., Dan
REGISTRION NUMBER: 22702
TELEPHONE: (816) 474 + 9050
TELEPHONE: (816) 474 + 9050
TELEPHONE: (816) 474 + 9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Plasmodium falciparum
US-09-140-466-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 FNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 462 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.4'
Best Local Similarity 72.2'
Matches 13; Conservative
                  APPLICANT: CLOUGH, BARBARA APPLICANT: PREISER, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 64106
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                              APPLICANT: WILSON, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
LENGTH: 410
```

ð

us-09-488-737-1.rai

```
Sequence 19, Application US/08454439

Patent No. 5591618

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADMINITY O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois
                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: DS/08/454,439 FILING DATE: 30-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB
Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-WAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: 08/123,932
17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-221-817-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-454-439-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression Cloning In
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09174768

Patent No. 625185

GENERAL INFORMATION:
APPLICANT: Muller, Sven
APPLICANT: Dalbage, Henrik
TITLE OF INVENTION: No. 6265185el Yeast Promoters Suitable For Expres
TITLE OF INVENTION: No. 6265185el Yeast Promoters Suitable For Expres
TITLE OF INVENTION: Heterologous Expression Of Proteins In Yeast
FILE REFERENCE: 4791.204-US
CURRENT FILING DATE: 1998-110-19
EARLIER FILING DATE: 1996-05-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 4; Length 460;
Pred. No. 2.8;
                                                                                                                                                                                                                                                          DB 6; Length 462
Patent No. 5225348

Patent No. 5225348

APPLICANT: HAGATA, SHIGEKAZU; SUGANO, SUMIO; KIM, DONG W.;
SUBTSUKI, TAICHI; KAZIRO, YOSHITO

TITLE OF INVENTION: DNA FRAGMENT AND EXPRESSION PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                        Score 51; DB (
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                     CONTAINING THE DNA FRAGMENT

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/447,823

FILING DATE: 08-DEC-1989
                                                                                                                                                                                                                                                        41.5%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.78;
60.08;
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.7
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                              7 RTKPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                    3 KEKTHINIVVIGHVD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 RTKPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KEKTHVNLVVIGHVD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: EF-lalpha
US-09-174-768-4
                                                                                                                                                                                   LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-174-768-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: (STATE:
                                                                                                                                                                SEQ ID NO:1
                                                                                                                                                                                                  5225348-1
                                                                                                                                                                                                                                                                                                                               ò
```

ŏ q

ö

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chanty, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49; DB 1; Length 689;
pred. No. 6.3;
6; Mismatches 3; Indels
                                                                                               DB 5; Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Felease #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/221,817
                                                                                               Score 49; DB
Pred. No. 6.3;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NOTE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEFORMER: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 18, Application US/08454439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.8%;
                                                                                               39.8%;
43.8%;
                                                                      Query Match
Best Local Similarity 43.5-
T; Conservative
                                                                                                                                                                                                                         342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.8
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                          5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-221-817-18
protein
; MOLECULE TYPE:
PCT-US94-10487-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-454-439-18
                                                                                                                                                                                                                                                                                                                                        US-08-221-817-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application PC/TUS9410487
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606

ZIP: 60606

MEDIUM TYER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 1
Pred. No. 6.3;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: NOLand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6408
TELEPX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
               ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELER: 25-3856
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:: ||| ::|| |::
342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-454-439-19
                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
PCT-US94-10487-19
```

g ò

```
5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-10487-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 60606
                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 16
US-08-221-817-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                APPLICANT: Chantry, David
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hockstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSE: Arshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US94-10487-18

Sequence 18, Application PC/TUS9410487

GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: ALEADRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
                                                                                                                                                                                                                                                                                                                       MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION NUMBER: US 08/221,817
APPLICATION NUMBER: US 08/221,817
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STAME: Llinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NO. 5511618and, Greta B. REGISTRATION NUMBER: 35,302
REFERENCE/FOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 SEP 1993
NI: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 689 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 43.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                  ZIP: 60606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                    GENERAL INFORMATION:
Patent No. 5591618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-454-439-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
TITLE OF INVENTION: A No. 553215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB :
Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 17 SEP 1993
CLASSIFICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
NAME: NOIANG GREAR E
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37866/31981
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6300
TELECHONE: (312) 474-6448
TELECHONE: (312) 474-6448
TELECHONE: (312) 474-0448
TELECHONE: (312) 474-0448
TELECHONE: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 689 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 FSKKKPHASVGTHGYM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 43.8
Matches 7; Conservative
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application PC/TUS9410487

Sequence 20, Application PC/TUS9410487

GENERAL INFORMATION:
TTILE OF INVENTION: A Novel G Protein-Coupled Receptor TITLE OF INVENTION: A Novel G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: G130 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
COUNTRY: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US94/10487
FILING DATE:
FILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 699;
                                                                                                                                                   Score 49; DB 1; Length 699;
Pred. No. 6.4;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.8%; Score 49; DB 5
43.8%; Pred. No. 6.4;
Live 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27866/31981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 17 SEP 1993
FILING DATE: 17 SEP 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INPORMATION:
NAME: NOLand, Greta E.
REGISTRATION UNDRER: 35,302
REFERENCE/DOCKET UNBER: 2786
TELECOMMUNICATION INFORMATION:
TELEFRA: (312) 474-0448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
                                                                                                                                                   Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                    143 FSKKKPHASVGTHGYM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                 5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10487-20
                            ; MOLECULE TYPE: protein US-08-454-439-20
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
PCT-US94-10487-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08454439

Sequence 20, Application US/08454439

Batent No. 5591618

GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: A No. 5591618e1 G Protein-Coupled Receptor TITLE OF INVENTION: Kinase GRK6

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Borun
STRRET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 1; Length 699;
Pred. No. 6.4;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: DOBOUGE
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/21,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
APPLICATION NUMBER: 35,302
RESISTRATION NUMBER: 35,302
RESISTRATION NUMBER: 35,302
RESISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RELEPONE: (312) 474-6300
TELEPAX: 55-986
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                      ATTORNEY AGENT INFORMATION:
NAME: NO. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31,302
RELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEPHONE: (312) 474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 39.8%;
Best Local Similarity 43.8%;
Matches 7; Conservative
   FILING DATE: 17 SEP 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 699 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:: ||| ::|| |::
| 343 FSKKKPHASVGTHGYM 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 FNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-221-817-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-454-439-20
```

ò g

```
RESULT 21
US-092735654
US-273-565-40
Sequence 40, Application US/09273565A
Patent No. 6166190
GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: HORIE, MASARSHI
APPLICANT: HORIE, MASARSHI
APPLICANT: HORIE, MASARO
TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZIME
FILE REFERENCE: 0-5359
CURRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER FILING DATE: 1999-03-22
EARLIER FILING DATE: 1999-03-22
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PAPENTICATION NUMBER: 20
SOFTWARE: PAPENTICATION NUMBER: 21
SEQ ID NO 40
LENGTH: 499
TAVEN: NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 499;
6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48; DB 3
Pred. No. 6.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB Pred. No. 6.3; 1; Mismatches
      APPLICATION NUMBER: US/09/055,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
US-09-565-538-40
; Sequence 40, Application US/09565538
; Patent No. 6333404
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,170
                                                                                                                       APPLICATION
FILING DATE:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFX: (491103
TELEFX: 6491103
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-055-699-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||: |||||
72 KEHVNVFIGHVD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-273-565-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 KEHVNVVFIGHVD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
US-08-21-170A-40

| Sequence 40, Application US/08820170A
| Patent No. 5831058
| GENERAL INFORMATION:
| APPLICANT: Tsutomu, FUJIWARA
| APPLICANT: Takeshl, WATANABE
| APPLICANT: Toyomasa, KATAGIRI
| TITLE OF INVENTION: HUMAN GENE
| NUMBER OF SEQUENCES: 42
| CORRESPONDENCE ADDRESS:
| STREET: 2100 Pennsylvania Avenue, N.W. CAPATE. SAPATE. |
| CORRESPONDENCE SUGINUE, Mino, Zinn, Macpeak & Seas
| STREET: 2100 Pennsylvania Avenue, N.W. CAPATE. |
| CORRESPONDENCES: | CORRESPONDENCES: | CORRESPONDENCES: |
| CORRESPONDENCES: | C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.0%; Score 48; 69.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/820,170A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/09055699; Patent No. 6005088; GENERAL INFORMATION: APPLICANT: Tautomu, FUJIWARA APPLICANT: Takeshi, WATANABE APPLICANT: Toyomasa, KATAGIRI; TILLE OF INVENTION: HUMAN GENE NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELERAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 499 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C. COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C. COUNTRY: United States ZIP: 20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-170A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||: |||||
72 KEHVNVVFIGHVD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 20
US-09-055-699-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
```

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chenter
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadlphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 5; Length 480;
Pred. No. 18;
3; Mismatches 6; Indels
                                                                                                                                     Length 480;
                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                 Score 45; DB 2;
Pred. No. 18;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICALLON

PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,255
FILING DATE: 08-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UPN-1795
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPRORE (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 25
US-09-442-100-11
; Sequence 11, Application US/09442100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 47.15,
Best Local Similarity 47.15,
Best Local Similarity 47.15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :| ||: |||||
237 EEPTSRLSPHLKFGTIG 253
                                                                                                                                                                                                                                                      :| :| ||: ||||
237 EEPTSRLSPHLKFGTIG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIG 18
                                                                                                                                     Query Match
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-272-255-12
    single
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                PCT-US95-08565-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-08565-12
                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12. Application US/08272255

Fatent No. 5824659

GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Blue Light Photoreceptors of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
COUNTRY: USA
                                          TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME FILE REFERENCE: Q-53599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,255
FILING DATE: 08-7UL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 4;
Pred. No. 6.3;
1; Mismatches
                                                                                                    CURRENT PILIANG DATE: U3/39/39
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 09/27,565
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR PLING DATE: 1999-03-29
PRIOR PLING DATE: 1999-04-07
PRIOR PLING DATE: 1997-03-19
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR APPLICATION NUMBER: 08/820,170
PRIOR PILING DATE: 1997-03-19
PRIOR PILING DATE: 1996-03-19
PRIOR PLING DATE: 1996-03-19
PRIOR FILING DATE: 1996-03-19
PRIOR PRIOR DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFFWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UPN-1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATTON UNBABER: 36.317
REFERENCE/DOCKET UNBABER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568-3100
TELEPAN: (215) 568-3100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.0%;
69.2%;
  WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 480 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.0
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-565-538-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 KPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |||: |||||
72 KEHVNVVFIGHVD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

Gaps

```
GENERAL INFORMATION:
APPLICANT: Helle MD, Brian
APPLICANT: Helle MD, Brian
APPLICANT: Jenison, Steve
TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
TITLE OF INVENTION: the HARDS Virus.
CURRENT APPLICATION NUMBER: US/09/106,075A
CURRENT APPLICATION NUMBER: 08/210,762
PRIOR FILING DATE: 1994-03-22
PRIOR FILING DATE: 1993-10-26
PRIOR FILING DATE: 1993-10-26
PRIOR FILING DATE: 1993-09-13
PRIOR FILING DATE: 1993-09-13
PRIOR FILING DATE: 1993-09-13
PRIOR FILING DATE: 1993-09-25
NUMBER OF SEQ ID NOS: 90
SOSTWARE PARCENT PARCENT NUMBER: 08/111,519
PRIOR FILING DATE: 1993-08-25
SOSTWARE PARCENT PARCENT NUMBER: 08/111,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1148;
                                                                                                                                                                                                                                                                                                                                                                                       Length 1142;
                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 4; Length 114
Pred. No. 1.5e+02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GICNAC '2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE SACS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.1%; Score 42; DB 4; Le illarity 31.6%; Pred. No. 1.5e+02; Conservative 6; Mismatches 7;
       08/111,519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 90, Application US/09106075A; Patent No. 6316250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/08626994A; Patent No. 5798244
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1993-08-25
NUMBER OF SEQ ID NOS: 90
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                          34.1%;
                                                                                                                                                                                                                                   ) ORGANISM: Prospect Hill virus US-09-106-075A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || |:||: |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : || |:||:: : |
934 QSFNVTEPHISTSALEWID 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EKFNRTKPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKFNRTKPHVNIGTIGHVD 21
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.1
Best Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Puumala virus
US-09-106-075A-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-106-075A-90
                                                                                                                                                                                LENGTH: 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-626-994A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 90
                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 89, Application US/09106075A
Patent No. 6316250
GENERAL INFORMATION:
APPLICANT: Hielle MD, Brian
APPLICANT: Hielle MD, Brian
APPLICANT: Hielle MD, Brian
APPLICANT: Hollson, Steve
TITLE OF INVENTION: the HARDS Virus.
FILE REFERENCE: 10312-801, Hielle et al. (210312.0009)
CURRENT APPLICATION NUMBER: US/09/106,075A
CURRENT FILING DATE: 1994-03-22
PRIOR FILING DATE: 1994-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                         APPLICANT: Xu, Tian
APPLICANT: Tao, Wufan
APPLICANT: Hang, Weiyi
APPLICANT: Wang, Sheng
APPLICANT: Yu, Wan
TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF LATS
TITLE OF INVENTION: GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 620;
74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/442,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 74;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET NUMBER: 6523-003
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42;
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CIIY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: 08/120,096
1993-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08/141,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.1%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1994-03-22
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1993-10-26
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1993-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 620 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 34.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-442-100-11
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 NRTKPHVNIGT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | :||:|:||
3 NTNRPHLNLGT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
                                GENERAL INFORMATION:
   Patent No. 6359193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-106-075A-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 364;
                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-
TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; Score 41; DB 40.0%; Pred. No. 59; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                33.3%; Score 41; DB 40.0%; Pred. No. 54; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: 18 C compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PEFFECT 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: APRII 3, 1996
CLASSIFCATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: APRII 3, 1995
ATTORNEY ARENT INFORMATION:
NAME: AROLI TURK
REGISTRATION NUMBER: 33,094
REGISTRATION NUMBER: 33,094
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08626994A Patent No. 5798244
TELEPHONE: (703) 716-1191
; TELEFAX: (703) 716-1180
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-08-957-742-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 716-1191
TELEFAX: (703) 716-1180
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 40.09
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.3
Best Local Similarity 40.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1941 Rola CITY: Reston STATE: Virginia COUNTRY: U.S.A. ZIP: 20191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 30
US-08-626-994A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vuery Match 33.3%; Score 41; DB 1; Length 339; Best Local Similarity 40.0%; Pred. No. 54; Matches 8; Conservative 4; Mismatches 0 - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-957-742-3
Sequence 3, Application US/08957742
Sequence 10. 60171743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-TITLE OF INVENTION: SIA' 2,3Gala 1,4GlCNAC '2,8-TITLE OF INVENTION: SIA' 2,3Gala 1,4GlCNAC '2,8-TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Greenblum & Bernstein, P.L.C. STREET: 1941 Roland Clarke Place CTTY: Reston STATE: Virginia COUNTRY: U.S.A.
                          COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: In4 pc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,994A
FILING DATE: April 3, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/1995
FILING DATE: April 3, 1995
ATTORNEY AGENT INFORMATION:
NAME: ALD TURK
RESISTATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDRER: 08/626,994
FILING DATE: APT11 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: APT11 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: AROLI TURK
REGISTATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PELÍCET 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 KNFSLTKSSVRIGQLMHYDY 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-626-994A-3
```

g à

```
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
TITLE OF INVENTION: IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/039,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40.5; DE
Pred. No. 62;
5; Mismatches
                                                                                                                                                                          FILING DATE: 16 MAR-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,623
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70275
TELECHOME: 610-407-0700
                                                                                                                   минек: US/09/039,609
16-мак-1998
N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1488-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08646981; Patent No. 5852183; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||: :| || |: ||||
279 VKEELPQERPAVN-QTVAEVDH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KINACHI, KAZUHIKO
APPLICANT: ONO, YOLCHI
APPLICANT: TOKIYOSHI, SACHIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEINER, MARC S REGISTRATION NUMBER: 32, REFERENCE/COKET NUMBER: INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Sir
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
US-08-646-981-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-039-609-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 364;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                      Sequence 1, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC '2,8-TITLE OF INVENTION: SIALYLTRANSFERASE
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
US-09-039-609-4
; Sequence 4, Application US/09039609
; Patent No. 6107473
; GENERAL INFORMATION:
APPLICANT: ALBONE, EARL
APPLICANT: RIKLY, KRISTINE
TITLE OF INVENTION: HTHB247
; NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Rather & Prestia
STREET: P.O. BOX 980
; CITY: Valley Forge
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum & Bernstein, P.L.C.
STREET: 1941 Roland Clarke Place
CITY: Reston
STATE: Virginia
COUNTRY: U.S.A.
ZIF: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
COMPUTER: MS-COMPUTER: MS-COMPUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%; Score 41; 40.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435 '
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: JP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: ATDOID TURK
REGISTRATION NUMBER: 33,094
REGISTRATION NUMBER: 33,094
REFERENCE/COCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
TELEPRAX: (703) 716-1191
TELEPRAX: (703) 716-1191
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 KNFSLTKSSVRIGQLMHYDY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.0v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19482
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-957-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΡA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: P
COUNTRY:
                         -08-957-742-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Gaps

ò g

```
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 3; Length 407; Pred. No. 96; 8; Indels 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 407;
96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENTIN STATEM.

SOFTWARE PATENTIN STATEM.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989;370

FILING DATE: 12-DEC-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MAKI, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.404C5

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED and BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 3
Pred. No. 96;
3; Mismatches
                                                  ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DCOKET NUMBER: 210121.404C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)62-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
STRANDEDNESS:
APPLICATION NUMBER: US/08/989,370 FILING DATE: 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08989370 Patent No. 6013268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.5%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                   32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKFNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EKFNRTKPHVNIGTIGHV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 38.99
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   Query Match 32.5
Best Local Similarity 38.9
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Columic CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                               linear
                     FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                             ;
US-08-989-370-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9-018-989-370-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-989-370-5
Sequence 5, Application US/08989370
Patent No. 6013268
GENERAL INFORMATION:
APPLICANT: Reed, Steven G,
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                      ö
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                   Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 4; Length 336;
Pred. No. 78;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACELLUIAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT FILING DATE: 1998-08-10
NUMBER OF SEO ID NOS: 5
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                 32.5%; Score 40; DB 2; 45.0%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                               US-09-131-648-1; Sequence 1, Application US/09131648; Patent No. 6168920; GENERAL INFORMATION:
                                                                                                                                                                                                                                                              178 EEQFNGTYRVVSVLPIGHQD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%;
50.0%;
                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVD 21
                 LENGTH: 334 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                              Query Match
Best Local Similarity 45.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: 2635136
US-09-131-648-1
                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-646-981-16
 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|: ||||| |:
99 RFHTTKPHVICNTL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

qq

à

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                            Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 4; Length 508; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KIENY, Marie-Paule
APPLICANT: KIENY, Marie-Paule
TITLE OF INVENTION: MOVEL HYBRID, SOLUBLE AND UNCLEAVED
TITLE OF INVENTION: gp160 VARIANT
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
CUNTRY: Uniqinia
COUNTRY: Uniqinia
COUNTRY: Uniqinia
ZIP: 22313-1404
                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US
FILING DATE: 31-DEC-1992
ATTONEY/AGENT INFORMATION:
ANNUMBERY DATE: ATTOMATION:
ANNUMBERY DATE: ATTOMATION:
                                                                                                                                                                                            Score 40; DB 3; 1
Pred. No. 1.1e+02;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 474
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-055
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 22, 2002, 07:44:32
                                                                                                                                                                                                                                                                                                                                                                                                      US-08-472-240A-16; Sequence 16, Application US/08472240A; Patent No. 6284248; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.5%;
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508 amino acids
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                        :||| | |: |:
186 KKFNGTGPCTNVSTV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||| | | |: |:
232 KKFNGTGPCTNVSTV 246
                                                                                                                                                                                                                                                                                3 EKFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-472-240A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                        ; ORGANISM: HIV
US-08-889-841B-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-00-889-841B-36

Sequence 36, Application US/08889841B

GENERAL INFORMATION:

TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE

FILE REFERENCE: 14918-703CIP

CURRENT APPLICATION NUMBER: US/08/889,841B

CURRENT FILING DATE: 1997-07-08

PRIOR RPLICATION NUMBER: US 60/676,737

PRIOR PRICE 11996-07-08

NUMBER OF SEQ ID NOS: 57

SOFTWARE: F8stSEQ for Windows Version 3.0

SEQ ID NO 36

LENGTH: 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 3; Length 455;
Pred. No. 1.1e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 3; Length 474 Pred. No. 1.1e+02; 3; Mismatches 5; Indels
                                                                                                                                                               APPLICANT: BERNAIN, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
RIOR APPLICATION NUMBER: US 60/676,737
PRIOR PELLING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berman, Phillip W.
TITLE OF INVERVIEW. HIV EVIDEDE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1996-07-08
                                                                                  RESULT 37
US-08-989-841B-46
Sequence 46, Application US/08889841B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
US-08-889-841B-39
: Sequence 39, Application US/08889841B
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.58;
  Query Match 32.5
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.5
Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||| | |: |:
189 KKFNGTGPCTNVSTV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| | | |: |:
186 KKFNGTGPCTNVSTV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EKFNRTKPHVNIGTI 17
                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: HIV
US-08-889-841B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: HIV
US-08-889-841B-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Job time: 91 sec

			191			
					e	
						•

of transl on factor of transl

of elfamy protein f ccus faeca

us-09-488-737-1.rag

ı

protein

.. 0

Run ĕ

Sequence:

Searched:

Database

```
Zea mays protein f
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Candida ablicans e
Arabidopsis thalia
Bitchondrial EF-T
Human prostate can
Novel human enzyme
Sequence of transi
Plasmodium falcipa
Drosophila melanog
                                                                                                                                                                                                                                                                                           Putative P. abyssi
Human cancer assoc
Human cancer associ
Lung cancer associ
Novel human diagno
Novel human secret
Novel human diagno
Novel human diagno
Novel human diagno
Novel human diagno
Lung cancer associ
                           Sequence of transl Sequence of elfamy Sequence of elfamy Sequence of elfamy Sequence of elfamy Sequence of elfamy
                                                                                    Chlamydia pneumoni
C. pneumoniae CT32
C. trachomatis CT3
Protein involved i
Propionibacterium
                                                                                                                  S. epidermidis ope
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
                                                                  Enterococcus faeca
Enterococcus faeca
Propionibacterium
Chlamydia pneumoni
                                                                                                                                                                                                                                                                                                                                                                     Breast and ovarian
Novel human diagno
Novel human diagno
            Streptococcus pneu
Sequence of transl
                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis t
Arabidopsis t
Arabidopsis t
Arabidopsis t
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis
Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis
Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis
                        Elongation
                                                            Zea mays
                                                                                                                                                                                                                                                                                                                                                                                        Novel
AAU36402
AAU37549
AAR20423
AAR20245
AAR20245
AAR20245
AAR20245
AAR20246
AAR20246
AAR30340
AAU3699
AAU38909
                                                                                                                                                                                                                                                 AAG34903
ABB50268
AAB56937
AAU23533
AAR20244
                                                                                                                                                                                                                                                                                                   AAB44062
AAG75706
AAB58481
                                                                                                                                                                                                                                                                                                                     ABG19061
AAB96700
ABG11316
AAU32988
ABG11419
ABG19062
AAB58508
AAB58508
AAB58722
ABG17756
ABG22108
                                                                                                                                                                                                                                                                                                                                                                                             AAG35976
AAG33972
                                                                                                                                                                                                                                                                                                                                                                                                         AAG35974
AAG37127
AAG37126
AAG35134
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG23949
AAG25187
AAG32345
AAG35730
                                                                                                                                                                                                                                                                                AAE07211
ABB58293
                                                                                                                                                                                                                                                                                             AAB96210
                                                                                                                                                                                                                                                                                                                                                   36802
2000
2000
36802
36802
36802
36802
36803
36803
36803
4693
4693
4693
$\text{Constraints}$
2244444444
 Helicobacter pylor
Helicobacter pylor
Helicobacter pylor
E. coli proliferat
E. coli cellular p
Haemophilus influe
Haemophilus influe
Salmonella typhi c
                                                                                                                                                                                   N-terminal sequenc
                                         August 22, 2002, 07:43:01 ; Search time 51.87 Seconds (without alignments) 47.111 Milljon cell updates/sec
                                                                                                                                                                                                                                                                                                                                 results predicted by chance to have a . to the score of the result being printed of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                             Description
      4.5
Compugen Ltd
                                                                                                                        hits satisfying chosen parameters:
                                                                                                             747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
      GenCore version Copyright (c) 1993 - 2000
                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                         AAU35822
AAB15890
AAU34769
AAU34838
AAU35466
AAU35476
AAU38371
AAG93183
                                                                                                                                                                                                                                                                                                                                                                                             AAW73036
AAW73035
                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                        AAW33404
                                                                              1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of res
score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                               A_Geneseq_032802:*
                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                        US-09-488-737-1
                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                     Query
                                                                                                                                                                                                                                                                                                                                                                                       1000.0
1000.0
995.9
990.2
990.2
860.2
860.2
                                                                                                                                                                                            rotal number of
                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                             123
118
118
111
1111
1111
1111
1111
                                                                                          Scoring table:
```

thalia thalia thalia thalia thalia

thalia

diagno

human

Result No.

2 4 4 7 7 8 9 9 11 10

us-09-488-737-1.rag

```
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Zea mays protein f
                                                                  Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                          Zea mays protein f
Human secreted pro
Zea mays protein f
Zea mays protein f
                                                                                                                                                    Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified Helicobacter pylori proteins are obtained from a membrane fraction and have apparent molecular weights (by electrophoresis on= 10% polyacylamide gel in presence of SDS) of 54, 50, 32-35 and 30 kD respectively, of which the 54 kD protein does not react with anti-catalase antiserum. The present sequence represents the Verminal of the 50 kD protein. The proteins and purified peptides derived from them can be used (by active immunisation) to treat or prevent H. pylori infections (gastritis, peptic ulcers, gastric cancer etc.). Antibodies raised against the protein can be used for psssive immunisation. Derived peptides and antibodies are also useful as reagents for diagnostic immunoassays, and antibodies are further useful for affinity purification of the new proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Helicobacter pylori membrane proteins - and related polypeptide(s) and antibodies, useful for active or passive immunisation and diagnosis
                                                                                                                                                                                                                                                                                                           membrane protein; vaccine; immunisation; immunoassay;
diagnostic; affinity purification; gastritis; peptic ulcer;
gastric cancer.
                                                                                                                                                                                                                                                                                            N-terminal sequence of 50 kD membrane protein of H. pylori.
                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
                                                                                                                              AAG35256
AAG35255
AAG24689
                                                AAG47135
AAG12390
                                                                                       AAG23943
AAG46906
                                                                                                           AAG12391
AAG03900
                               AAG47136
AAG47144
                                                                    AAG23944
AAG46907
AAG45353
AAG45356
                   AAG45359
                                                                                                                                                                                                                                peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 30; 48pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                96WO-FR01552.
                                                                                                                                                                                                                                                                                                                                                                                                                                   95FR-0011890
                    22222222222222222
                                                                                                                                                                                                                                                                        (first entry)
                   4449
4449
1150
1150
1133
1110
464
465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-226163/20.
                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
                                                                                                                                                                                                                                AAW33404 standard;
22 AA
                                                                                                                                                                                                                                                                                                                                                                        WO9712909-A1
                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-1995;
                                                                                                                                                                                                                                                                        05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1997
Lissolo L;
                                                                                                                                                                                                                                                     AAW33404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                        AAW33404
 RESULT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the N-terminal sequence of a 50 kDa protein, designated GHPO 750, isolated by immunoaffinity chromatography from a membrane fraction of Helicobacter pylori ATCC 43579. The invention provides Helicobacter polypeptides (see AAN73022-32 and AAN33034-35) and polynucleotides (see AAN72001, AAN07912-11 and AAN07963-64) that can be used in methods for the treatment and prevention of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases
                                                                                                                                                                                                                             Infection; gastritis; ulcer; vaccine; diagnosis; therapy.
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 22;
22;
                                                                                                                                                                                                    Helicobacter pylori 50 kDa polypeptide N-terminal peptide.
 Length
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
(INNR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Miller C,
100.0%; Score 123; DB 18; 100.0%; Pred. No. 4.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 123; DB 19;
100.0%; Pred. No. 4.9e-13;
tive 0; Mismatches 0;
                        ö
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Lissolo L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1.C.4; Page 56; 184pp; English.
                                                                                                                                                                                                                                                     Helicobacter pylori strain ATCC 43579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                  Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein; 399
                        ö
                                                           22
                                                                                                                                 AAW73036 standard; Peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                        Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                  97US-0834666.
97US-0831310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 mkekfnrtkphvnigtighvdh
                                               MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                            98WO-US06421
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-568251/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                      Al-Garawi A,
                                                                                                                                                                                                                                                                            WO9843479-A1
                                                                                                                                                                                                                                                                                                                            31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                  01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1999
                                                                                                                                                                               02-FEB-1999
                                                                                                                                                                                                                                                                                                    08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                        22;
Query Match
Best Local S:
Matches 22,
                                                                                                                                                         AAW73036;
                                                                                                                                                                                                                             HPO 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW73035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW73035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW73035
ID AAW7
XX
AC AAW7
XX
DT 02-F
                                                                                                                      AAW73036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                           RESULT
                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
```

Carr GJ;

ŏ

3

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aucreus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also used in featification of potential new targets invention is also used in proliferation, to express these proteins. To identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen correction in the proteins uncleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from a directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli, E. coli, proliferation, inhibition, screening, antimicrobial; bacterial growth, antisense therapy; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli proliferation associated protein sequence SEQ ID NO:247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 399;
                                                                                                                                                                                                                                                                                                                                                                        Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 118; DB 22;
Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                        Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 11415; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 7.7
Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB15890 standard; Protein; 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.9%; Sc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 kekfnrtkphynigtighydh 23
                                                                                                                                                                      2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                           21-MAR-2001; 2001WO-US09180.
                                                                                                                                                    2000US-191078P
                                                                                                                                                                                                                                                                                      16-FEB-2001; 2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHV
                                                                                                                                                                                                                                                                                                                                                                                               Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-611495/70.
N-PSDB; AAS53681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AA;
                    WO200170955-A2.
                                                                                                                                                                                             26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                            famamoto RT,
                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
                                                                                                                                                                             23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2000
                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB15890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB15890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŊΕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of a 50 kDa Helicobacter pylori polypeptide designated GHPO 750. It was deduced from an isolated genomic DNA sequence (see AAVV)963). The invention provides a family of 76 kDa Helicobacter polypeptides (see AAW73022-32), as well as GHPO 750 and a 32 kDa polypeptides (see AAW73034), and also polynucleotides (see AAV72001, AAVV912-21 and AAVV953-64) encoding them, expression cassettes, and methods for producting the unprocessed mature polypeptides in host cells. The polypeptides can be used in waccination methods to prevent or treat Hb Infection in a mammal. Methods and products of the invention allow treatment and prevention of gastroduodenal diseases associated with Hb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastroduodenal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections, including aucte, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. Detection and diagnostic methods are also provided. GHPO 750 was demonstrated to be a protective antigen. Unlike the other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         demonstrated to be a protective antigen. Unlike the other polypeptides of the invention, GHPO 750 is not a secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.9%; Score 118; DB 19; Length 399; 100.0%; Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                        Tomb J;
                                         GHPO 750; infection; gastritis; ulcer; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
(INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS ET VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori cellular proliferation protein #135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation protein antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                   Al-Garawi A, Kleanthous H, Lissolo L, Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
Helicobacter pylori 32 kDa polypeptide GHPO 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 150-152; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU35822 standard; Protein; 399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 kekfnrtkphvnigtighvdh 23
                                                                                                                                                                                                                                                                                   97US-0834666.
                                                                                                                                                                                                                                          98WO-US06421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-568251/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV07964
                                                                                                                                                    W09843479-A1
                                                                                                                                                                                                                                          31-MAR-1998;
                                                                                                                                                                                                                                                                                   01-APR-1997;
01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-FEB-2002
                                                                                                                                                                                               08-OCT-1998
```

Sequence

Query Match

ò g AAU35822

AAU35822 RESULT

ö

Gaps

Carr GJ;

oţ

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Rlebsiella pneumoniae, Pseudomonas aeruqinosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids squence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Oct. The sequence data for this patent did not form part for the printed specification, but was obtained in electronic
                                                                                                                                                                    Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 111; DB 22; 90.5%; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli cellular proliferation protein #419
                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 10362; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1e-0
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                    Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU34838 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                   23-0CT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-191078P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                    Ohlsen KL,
                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                 WPI; 2001-611495/70.
                                                                                                                                                                                          Xu HH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli.
                                                                                                                                                                                                                                                    N-PSDB; AAS52628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200170955-A2.
                                                                                                                                                                                          famamoto RT,
                                                                                                                                                                    Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU34838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU34838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAA66055 and AAB15806 to AAB16060 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66057 represent pimers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention can be used to identify a proliferation. required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory inhibition occurs in the second microorganism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
                                                                                                                                                                                                                                                      Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                    Ohlsen KL, Trawick J, Forsyth RA, Froelich JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.2%; Score 111; DB 21; Length 394; 90.5%; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E. coli cellular proliferation protein #350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 177-178; 316pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU34769 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001WO-US09180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
                                                                                                                         27-JAN-2000; 2000WO-US02200
                                                                                                                                                                  99US-0117405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                  Zyskind J, Ohlsen K
Yamamoto RT, Xu HH;
                                                                                                                                                                                                                                                                                                            2000-514822/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 AA;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAA65894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                      WO200044906-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170955-A2.
                                                                                                                                                                  27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002
                                                                                  03-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU34769;
```

9

g

õ

AAU34769

ö

Gaps

Ŋ

```
21-MAR-2001; 2001WO-US09180.
                                                                                                         Haselbeck R,
                                                                                                                   Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU35476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU35476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The Invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                             Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                            New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.2%; Score 111; DB 22; Length 394; 90.5%; Pred. No. 1e-09; 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae cellular proliferation protein #107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                            Example 3; Seq ID No 10431; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU35466 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 kekfertkphynygtighydh 23
                   2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                      format directly from WIPO at
          2000US-207727P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae
                                                                                                         Xu HH;
                                                                                                                             WPI; 2001-611495/70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   394 AA;
                                                                                                                                        N-PSDB; AAS52697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200170955-A2.
                                                                                              Haselbeck R,
                                                                                                        Yamamoto RT,
                                                   16-FEB-2001;
                   23-OCT-2000;
27-NOV-2000;
                                        22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2002
          26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU35466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU35466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
```

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premmoniae, Pseudomonsa aeruginosa and Enterococcus faecalis. The commoniae, Pseudomonsa aeruginosa and Enterococcus faecalis. The commoniae, pseudomonsa aeruginosa and Enterococcus faecalis. The contabiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Con the printed specification, but was obtained in electronic form part form the directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                      Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Length 394;
                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae cellular proliferation protein #117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                      Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 111; DB 22
Pred. No. 1e-09;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 11059; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU35476 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 kekfertkphvnvgtighvdh 23
2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%;
llarity 90.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                          (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS53325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170955-A2.
                                                     26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
```

9

```
21-MAR-2001; 2001WO-US09180.
                                                                                                                                           Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1108790-A2.
                                              26-MAY-2000;
                                                         23-OCT-2000;
                                                                     27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2001
                        21-MAR-2000;
                                   23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG93183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG93183
  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klebsiella proemoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expresse proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an automorate data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                   New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 111; DB 22; Length 394; 90.5%; Pred. No. 1e-09; 1; Mismatches 1; Indels (
                                                                                                                                Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhi cellular proliferation protein #262.
                                                                                                                                                                                                                                      Example 3; Seq ID No 11069; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               format directly from WIPO at
ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU38371 standard; Protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 kekfertkphynygtighydh 23
                   20000S-206848P.
20000S-207727P.
20000S-242578P.
20000S-253625P.
20000S-257931P.
            2000US-191078P
                                                                                2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.2%
Best Local Similarity 90.5%
Matches 19; Conservative
                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                            Xu HH;
                                                                                                                                                                 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi
                                                                                                                                                                             N-PSDB; AAS53335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200170955-A2.
                                             23-OCT-2000;
27-NOV-2000;
                                                                                16-FEB-2001;
                                                                                                                             Haselbeck R,
Yamamoto RT,
                                   26-MAY-2000;
                                                                     22-DEC-2000;
                       23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU38371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU38371
δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                         Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                         Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.2%; Score 111; DB 22; 90.5%; Pred. No. 1.1e-09; iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                     Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C glutamicum protein fragment SEQ ID NO: 6937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 13964; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG93183 standard; Protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-207727P
                                                                                                                              2000US-253625P.
2000US-257931P.
2000US-191078P
                               2000US-206848P
                                                                                                                                                                                                    16-FEB-2001; 2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                     Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-611495/70.
N-PSDB; AAS56230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 AA;
```

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to reducify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part form the propertion, when the patent did not form part form the directly from MPO at
                                                                                                                                 Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                              of
-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106, DB 22; Length 397;
Pred. No. 6.7e-09;
1; Mismatches 2; Indels
                                                                                                                                 Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa cellular proliferation protein #399.
                                                                                                                                                                                                                                                              New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                 Wall D,
                                                                                                                                                                                                                                                                                                                              Example 3; Seq ID No 11995; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                 Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU36409 standard; Protein; 397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 kekfernkphynygtighydh 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2000; 2000US-191078P.
23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.77
Watches 18; Conservative
                                                                                                                                 Ohlsen KL,
                                                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                 WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 AA;
                                                                                                                                                                                                                     N-PSDB; AAS54261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200170955-A2
                                                                                                                                 Haselbeck R,
                                                                                                                                                      Tamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU36409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU36409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the examplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                     mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                              Novel polynucleotides derived from Coryneform bacteria, for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                 S, Hayashi M, Ochiai K, Yokoi H;
Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 29; SEQ ID NO: 6937; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa cellular proliferation protein #392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106; DB 22;
Pred. No. 6.6e-09;
0; Mismatches 2;
                                                                                                                                                                                                 Ando S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU36402 standard; Protein; 397 AA.
                                                                                                                                                                                                                     Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                   (KYOW ) KYOWA HAKKO KOGYO KK
                                                             16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                      18-DEC-2000; 2000EP-0127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002 (first entry)
                                                                                                                                                                                               Nakagawa S, Mizoguchi H,
Tateishi N, Senoh A, Ike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                              WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 AA;
                                                                                                                                                                                                                                                                                N-PSDB; AAH68402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU36402;
```

RESULT 12 AAU36402

ò g ó

Carr GJ;

œ

```
prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential comes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aurens, Salmonella typhi, Klebsiella C Escherichia coli, Staphylococcus and Enterococcus faecalis. The commoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The C invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. C and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen can wade variety of organisms. The present sequence represents an avide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

C Note: The sequence data for this patent did not form part of format directly from WIPO at the principal and directly from WIPO at the mino in the control of the principal and the control of the control of the principal and the control of the control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of translation elongation factor Tu2 encoded by tuf2 gene.
                                                                                                                                                                                                                   Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 398;
                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elfamycin resistant actinomycetes; antibiotic resistant; elongation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.2%; Score 106; DB 22;
85.7%; Pred. No. 6.7e-09;
tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Seq ID No 13171; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pūb/published_pct_sequences.
                                                                                                                                                                                                                 Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR20243 standard; Protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 kekydrskphvnigtighvdh 23
                         2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                       2001US-269308P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91EP-0201702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91EP-0201702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces ramocissimus.
                                                                                                                                                                                                                   KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                              (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                 Ohlsen
                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
N-PSDB; AAS55437.
                         23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                 Haselbeck R,
Yamamoto RT,
                                                                                                       16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP466251-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR20243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel annibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Conter The sequence data for this patent did not form part form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                          Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                          Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae cellular proliferation protein #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.2%; Score 106; DB 22;
85.7%; Pred. No. 6.7e-09;
iive 1; Mismatches 2;
                                                                                                                                                                                     Ohlsen KL, Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Seq ID No 12002; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU37578 standard; Protein; 398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 kekfernkphynygtighydh 23
                   2000us-253625P.
2000us-257931P.
2001us-269308P.
2000US-242578P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001WO-US09180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-191078P.
2000US-206848P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
                                                                                                                                                                                                                                                                   WPI; 2001-611495/70.
                                                                                                                                                                                                                 Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 AA;
                                                                                                                                                                                                                                                                                               N-PSDB; AAS54268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170955-A2.
                                                                                                                                                                                     Haselbeck R,
                                                  22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                              Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2000;
23-MAY-2000;
                           7-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU37578;
```

g ŏ

ö

Gaps

σ

ö

Gaps

ö

```
microorganism. This protein also has the ability to catalyse the transfer of aminoacyl-tRNA to a ribosome A site, and has a molecular weight of about 45 kD as determined by SDS-PAGE. The primers used to isolate the DNA encoding this sequence can also be used to detect the EF-Tu gene. The primers are also used for the highly accurate detection of microorganisms of the genus Lactobacillus, by specifically detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tuff encoding a protein, resistant to the elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufr) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence of translation elongation factor Tul encoded by tufl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΡW.;
                                                                                                                                                   Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heinstra
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Elfamycin resistant actinomycetes; antibiotic resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein conferring resistance to elfamycin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            வ்
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 13;
Pred. No. 2.9e-08;
2; Mismatches 2;
                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transform streptomycetes to resistant pheno-type
                                                                                                                                                     Score 103; DB 18;
Pred. No. 2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 1 and Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vijgenboom
                                                                                                                                                                                  Mismatches
                                                                                   the EF-Tu gene from these microorganisms
                                                                                                                                                                                                                                                                                                         Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bosch L,
                                                                                                                                                                                                                                                                                            AAR20242
ID AAR20242 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                               ï
                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                     24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.9%;
81.0%;
                                                                                                                                                      83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91EP-0201702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91EP-0201702
                                                                                                                                                                                                                          4 kehyertkphynigtighydh
                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces ramocissimus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Conservative
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kerkman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-017874/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                      Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  elongation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ20215
                                                                                                              396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGM,
                                                                                                                                                                                                                                                                                                                                                              15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP466251-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woudt LP;
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                    AAR20242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Luiten
                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                       δ
    à
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the elongation factor Tu (EF-Tu) of the invention. The DNA encoding this sequence was isolated from Lactobacillus paracasei subspecies paracasei using the primers shown in AAY92620 and AAT9261. This sequence is involved in the polypeptide chain elongation reaction in the blosynthesis of proteins in a Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tu; EF-Tu; Lactobacillus; polypeptide chain elongation;
sis; aminoacyl-tRNA transfer; ribosome A site; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                      valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein, resistant to the elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                          Substitution of residue 378 of the elongation factor (EF-Tu) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactobacillus polypeptide chain elongating factor Tu - used for detecting microorganisms belonging to the genus Lactobacillus
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                          Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                              Length 396;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                         used to
                                                                                                                                                                                                                                                                                                                                                             Score 105; DB 13;
Pred. No. 9.6e-09;
1; Mismatches 2;
                                                         Vijgenboom E,
                                                                                                                                                      transform streptomycetes to resistant pheno-type
                                                                                                                                         protein conferring resistance to elfamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactobacillus paracasei subspecies paracasei.
                                                                                                                                                                               Example; Pages 16-18; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW30303 standard; Protein; 396 AA.
                                                        ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 2-3; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                         Bosch
                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                              85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96JP-0059056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96JP-0059056
    90EP-0201851
                                                                                                                                                                                                                                                                                                                                                                                                                                  2 kakfqrtkphvnigtighidh
                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
                              (KONN ) GIST-BROCADES NV
                                                         Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation factor Tu;
protein biosynthesis;
                                                         Kerkman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elongation factor Tu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-520740/48.
N-PSDB; AAT92619.
                                                                                              WPI; 1992-017874/03
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                      396 AA;
                                                                                                             N-PSDB; AAQ20216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OZEK-) OZEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP09248186-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1996;
    10-JUL-1990;
                                                        Luiten RGM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-1997
                                                                                                                                                                                                                                                                                                                       Sequence
                                                                      Ľ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW30303;
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                       Woudt
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                         New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ö

Gaps

ó

RESULT

g

```
Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of elfamycin-resistant elingation factor EF-TuR Pro 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                    Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 102; DB 13; Length 3
Pred. No. 2.9e-08;
2; Mismatches 2; Indels
   Elfamycin resistant actinomycetes; antibiotic resistant; elongation factor.
                                                                                                                                                                                                                                                                                                                                             New protein conferring resistance to elfamycin - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elfamycin resistant actinomycetes; antibiotic resistant;
                                                                                                                                                                                                                                               Kerkman R, Bosch L, Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                           transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR20247 standard; Protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%;
81.0%;
                                                                                                                                          91EP-0201702
                                                                                                                                                                       91EP-0201702
90EP-0201851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91EP-0201702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91EP-0201702
90EP-0201851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 kakfertkphvnmgtighidh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                 Streptomyces ramocissimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces ramocissimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                  (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded by SrtufRi gene
                                                                                                                                                                                                                                                                                              WPI; 1992-017874/03.
N-PSDB; AAQ20219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elongation factor
                                                                                                                                          02-JUL-1991;
                                                                                                                                                                     02-JUL-1991;
10-JUL-1990;
                                                                                                                                                                                                                                                 Luiten RGM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1991;
10-JUL-1990;
                                                                                                             15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1992
                                                                              EP466251-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP466251-A.
                                                                                                                                                                                                                                                                   Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR20247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR20247
    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. Of elfamycin by actinomycetes is removed by mutating the gene tuf into tufR encoding a protein resistant to elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                     elfamycin-resistant elingation factor EF-TuR Val 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of elfamycin-resistant elingation factor EF-TuR Thr 378\, encoded by SrtufRl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                               Elfamycin resistant actinomycetes; antibiotic resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - nsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New protein conferring resistance to elfamycin - transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 102; DB 13;
Pred. No. 2.9e-08;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Pages 13-15; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                          AAR20245 standard; Protein; 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luiten RGM, Kerkman R, Bosch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR20246 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                   91EP-0201702.
                                                                                                                                                                                                                                                                                                                                                                      91EP-0201702
2 kakfertkphvnmgtighidh
                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                              Streptomyces ramocissimus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.9
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                  encoded by SrtufRl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-017874/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 AA;
                                                                                                                                                                                                                                               elongation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ20218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1991;
10-JUL-1990;
                                                                                                                                                     15-APR-1992
                                                                                                                                                                                    Sequence of
                                                                                                                                                                                                                                                                                                                                        15-JAN-1992
                                                                                                                                                                                                                                                                                                           EP466251-A.
                                                                                                                        AAR20245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR20246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                             AAR20245
```

AAR20246

RESULT

셤 ò

ö

Gaps

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                     Gaps
  1s
the limiting factor for the prodn. of elfamycin by actinomycetes removed by mutating the gene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TWR and the genes (tuff) encoding it.
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                       Length 396;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                    Query Match 82.9%; Score 102; DB 13; Best Local Similarity 81.0%; Pred. No. 2.9e-08; Matches 17; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays protein fragment SEQ ID NO: 50648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG40781 standard; Protein; 465 AA.
                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                            99US-0130449.
99US-0130510.
99US-0130891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0131449.
99US-0132048.
99US-0132407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0135353.
990S-0135629.
990S-0136021.
990S-0136392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0132486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0132863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0134218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0134941
99US-0135124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0128234
99US-0128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0132484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0134221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0130077
                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays subsp. mays.
                                                                                                                     AA;
                                                                                                                     396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1999
16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG40781;
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                              AAG40781
                                                                                                                                                                                                                                                                                                                               D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A CONTRACTOR OF THE CONTRACT O
    00000x8
                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                              Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that the limiting factor for the prodn. of elfamycin by actinomycetes is removed by mutating the agene tuf into tuff encoding a protein resistant to an elfamycin, pref. mocimycin (Kirromycin). The inventors claim EF-TuR and the genes (tufR) encoding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substitution of residue 378 of the elongation factor (EF-Tu) with a valine, threonine, proline or phenyalanine results in an elfamycin resistant protein (EF-TuR). The advantage of this change is that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of elfamycin-resistant elingation factor EF-TuR Pro 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heinstra PW;
                          Heinstra PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein conferring resistance to elfamycin - used to transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                 New protein conferring resistance to elfamycin - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elfamycin resistant actinomycetes; antibiotic resistant;
                          Vijgenboom E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bosch L, Vijgenboom E,
                                                                                                                                                                                           transform streptomycetes to resistant pheno-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 102; DB 13;
Pred. No. 2.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                     Claim 6; Pages 13-15; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                          Bosch L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR20248 standard; Protein; 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91EP-0201702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91EP-0201702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces ramocissimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KONN ) GIST-BROCADES NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by SrtufR1 gene.
                          Luiten RGM, Kerkman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luiten RGM, Kerkman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-017874/03.
                                                                                            WPI; 1992-017874/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elongation factor.
                                                                                                                     N-PSDB; AAQ20220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ20221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1991;
10-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP466251-A.
                                                Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR20248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woudt LP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR20248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
```

g

ò

9US - 0136782 9US - 0137528 9US - 0137528 9US - 0137502 9US - 0138640 9US - 0138847 9US - 013847 9US - 0139454 9US - 0139454 9US - 0139455 9US - 0139455	9905-0139458. 9905-0139459. 9905-0139460. 9905-0139461. 9905-0139462. 9905-0139463. 9905-0139817. 9905-0139817. 9905-014035. 9905-014035. 9905-014082. 9905-0141287. 9905-0142803. 9905-0142803.	90S - 0144085 90S - 1044086 90S - 1044325 90S - 0144331 90S - 0144333 90S - 0144334 90S - 0144334 90S - 0144336 90S - 0144336 90S - 0144336 90S - 014436 90S - 014638	90S-0145089 90GS-0145192 90GS-0145192 90GS-0145218 90GS-0145218 90GS-0145919 90GS-0145919 90GS-0145919 90GS-0146386 90GS-0146386 90GS-0146386
8 - MAY - 1999 3 - J. UUN - 1999 4 - JUN - 1999 7 - JUN - 1999 6 - JUN - 1999 6 - JUN - 1999 6 - JUN - 1999 6 - JUN - 1999 7 - JUN - 1999 8 - JUN - 1999 8 - JUN - 1999	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 22-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 26-JUN-1999; 26-JUN-1999; 27-JUN-1999; 28-JUN-1999; 29-JUN-1999; 20-JUL-1999; 20-JUL-1999; 21-JUN-1999; 21	5 - 7ur - 1999 6 - 101-1999 6 - 101-1999 9 - 7ur - 1999 9 - 7ur - 1999 9 - 7ur - 1999 9 - 7ur - 1999 9 - 7ur - 1999 1 - 7ur - 1999	2-UL 1999 3-UL 1999 3-UL 1999 3-UL 1999 3-UL 1999 7-UL 1999 8-UL 1999 8-UL 1999 3-AUC 1999 3-AUC 1999
7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2		9 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

90S - 0147302 90S - 0147192 90S - 0147260 90S - 0147303 90S - 0147403 90S - 0147403 90S - 0148171 90S - 0148311 90S - 0148341 90S - 0148684 90S - 0148684 90S - 0148684 90S - 0148684 90S - 0148684	905 01494 905 01494 905 01499 905 01499 905 01508 905 01508 905 01518 905 01519 905 01529 905 01554 905 01554 905 01554 905 01554 905 01554 905 01554 905 01554	0115753 01057865 01058230 011582369 01159236 01159239 01159230 01159239 01159239 01159239 01160740 0160740 0160815 0160989 0160989 0160989 0160989 0160989 0160989 0160989 0160989 0161920 0161920 0161920
04 - AUG - 199 05 - AUG - 199 05 - AUG - 199 06 - AUG - 199 06 - AUG - 199 10 - AUG - 199 11 - AUG - 199 13 - AUG - 199 13 - AUG - 199 13 - AUG - 199 17 - AUG - 199	R 20-AUG-1999 R 21-AUG-1999 R 21-AUG-1999 R 31-AUG-1999 R	

```
21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            famamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000;
                                                                                                                                                                                            14-FEB-2002
                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                   AAU34889;
               Query Match
                                                                                                                      24
                                                                                                                                 AAU34889
                                                                                                                       RESULT
                                                                                                                                                                     ò
                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotics used are becherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to dentify proteins used in proliferation, to express these proteins. The proteins antibodies capable of binding to the expressed proteins. The proteins are be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part for the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic ftp. wipo.int/pub/published_pct_sequences.
                         ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr GJ;
                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trawick JD,
Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                     Enterococcus faecalis cellular proliferation protein #27.
                       Indels
                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
Score 102; DB 21;
Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall
            Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Seq ID No 4887; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW,
                                                                                                                                AAU33391 standard; Protein; 395 AA.
                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
82.9%;
                                                                                                                                                                                                                                                                                                                                                               2000US-191078P
                                              4 KFNRTKPHVNIGTIGHVDH 22
                                                            21-MAR-2001; 2001WO-US09180
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Xu HH;
                       18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                  Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611495/70.
N-PSDB; AAS51250.
            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 AA;
                                                                                                                                                                                                                                                                                       WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
                                                                                                                                                                               14-FEB-2002
                                                                                                                                                                                                                                                                                                                27-SEP-2001
                                                                                                                                                       AAU33391;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                       Matches
                                                                                                                   AAU33391
                                               ò
                                                                    g
```

```
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are scherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella peumoniae, Pseudomonas aeruginosa and Enterococcus facefuls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acid sequence is also useful to screen can wise variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr GJ;
                                                                         Gaps
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oţ
          Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis cellular proliferation protein #176.
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
82.1%; Score 101; DB 22;
llarity 85.7%; Pred. No. 4.3e-08;
Conservative 2; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL, Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 10482; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                              AAU34889 standard; Protein; 395 AA.
                                                                                                                                     22
                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-206848P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-253625P
2000US-257931P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-191078P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-242578P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-269308P
                                                                                                                                                                      3 kekfdrskshvnigtighvdh
                                                                                                                                     2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-611495/70.
N-PSDB; AAS52748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu HH;
                                        Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2001;
```

```
132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                        W09927105-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1998;
                                                                                                                                                                                                                                                       13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Griffais R;
                                                                                                                                                                                                                             AAY34672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                        RESULT 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                      AAY34672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
  XX
So
                                                                                                                                 q
                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a cares. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The acness is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory resence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The note of presence or absence of P. acnes in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes polypeptides and charmed immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the Invibo.int/pub/published_pct_sequences.
                                                                 ö
                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endopthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                 .;
0
                                      Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhatia A;
                                                               1; Indels
                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #27410.
                                     Score 101; DB 22;
Pred. No. 4.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID No 27709; 1069pp; English.
                                                               Mismatches
                                                                                                                                                                                    AAU66514 standard; Protein; 132 AA.
                                                             2;
                                                                                                         3 kekfdrskshvnigtighvdh 23
                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                     82.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                        27-FEB-2002 (first entry)
                                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                    Best Local Similarity
395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS59738
                                                                                                                                                                                                                                                                                                                                                                                       WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2001.
                                                                                                                                                                                                             AAU66514;
 Sequence
                                     Query Match
                                                                                                                                                           RESULT 25
                                                                 Matches
                                                                                                                                                                        AAU66514
g
                                                                                           ð
                                                                                                                    g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 100; DB 20; Length 394;
Pred. No. 6.2e-08;
1; Mismatches 3; Indels
  Length 132;
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae transmembrane protein sequence.
                                                3;
Score 100; DB 22;
Pred. No. 1.8e-08;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 675; Disclosure; 1912pp; English.
                                                                                                                                                                                                                                                                       AAY34672 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; neutralising epitope.
                                                                                                22
                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.3%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-IB01890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0107078.
97FR-0014673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.0%;
                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-357842/30.
  Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 AA;
```

AAU38889 ID AAU3 XX

```
The invention relates to isolated polynucleotide encoding at least a partial Chlamydia protein which is an antigenic fragment, or the complements, fragments, homologues and variants, and antibodies raised against the antigenic proteins (or fragments). The nucleic acids, proteins and antibodies are used to diagnose and treat Chlamydia infections (e.g. a sexually transmitted disease, pelvic inflammatory disease (PID), acute respiratory tract infection, trachoma, atherosclerosis and coronary heart disease) in a patient, and in the treatment of male infertility. The compounds of the invention are also useful for detecting the presence of Chlamydia in a patient, and stimulating and/or expanding T cells specific for a Chlamydia protein. The present sequence represents a Chlamydia antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
Chlamydia; sexually transmitted disease; PID; antibacterial; pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein involved in transcription, translation and/or maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide for treating Chlamydia infections encodes a polynucleotides containing an immunogenic portion of a Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 22;
Pred. No. 6.2e-08;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 182-183; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Stromberg EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY36864 standard; Protein; 397 AA.
                                                                                                           Chlamydia trachomatis serovar D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.3%;
81.0%;
                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-198853P.
20-JUL-2000; 2000US-219752P.
                                                                                                                                                                                                                                     23-APR-2001; 2001WO-US13081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                   coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                     Bhatia A, Probst P,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-616771/71.
N-PSDB; AAS57041.
                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                    WO200181379-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1999
                                                                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY36864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY36864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide encoding at least a partial Chlamydia protein which is an antigenic fragment, or the complements, fragments, homologues and variants, and antibodies raised against the antigenic proteins (or fragments). The nucleic acids, proteins and antibodies are used to diagnose and treat Chlamydia infections (e.g. a sexually transmitted disease, pelvic inflammatory disease (PID), acute respiratory tract infection, trachoma, atherosclerosis and coronary heart disease) in a patient, and in the treatment of male infertility. The compounds of the invention are also useful for detecting the presence of Chlamydia in a patient, and stimulating and/or expanding T cells specific for a Chlamydia protein. The present sequence represents a Chlamydia antigen.
                                                                                                                                                                                                              pelvic inflammatory disease; antigen; trachoma; gynecological; acute respiratory tract infection; atherosclerosis; male infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide for treating Chlamydia infections encodes a polynucleotides containing an immunogenic portion of a Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 100; DB 22; Length 394;
Pred. No. 6.2e-08;
L; Mismatches 3; Indels (
                                                                                                                                                                                            Chlamydia; sexually transmitted disease; PID; antibacterial;
                                                                                                                                                  C. pneumoniae CT322 homologue CPn0074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 147; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΕΞ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU38909 standard; Protein; 394 AA.
                    AAU38889 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stromberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. trachomatis CT322 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.3%;
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2001; 2001WO-US13081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2000; 2000US-219752P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-198853P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ketfqrnkphinigtighvdh
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2002 (first entry)
                                                                                                                                                                                                                                                           coronary heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bhatia A, Probst P,
                                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-616771/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS57020
                                                                                                                                                                                                                                                                                                                                          WO200181379-A2.
                                                                                                         16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                              AAU38889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU38909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 28
```

NAMES OF THE PROPERTY OF THE P

ö

AAU38909

XEXEXEX

δ g

```
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO Syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequlate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies and also be used as diagnostic agents for determining P. acnes presence, for example, by once: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. epidermidis open reading frame protein sequence SEQ ID NO:1312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 22;
Pred. No. 6.9e-08;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                          Claim 6; SEQ ID No 1187; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG82109 standard; Protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 kakfertkphonigtighidh 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.3%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD
                      WPI; 2001-616774/71.
N-PSDB; AAS59510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-316495/33.
N-PSDB; AAH52959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG82109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                    AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, saplingitis, and perihepatitis, bartholinitis; pummopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 100; DB 20; Length 397;
Pred. No. 6.2e-08;
1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes immunogenic protein #888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW, Persing DH, Mitcham JL, Wang S.
L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 735-736; 1755pp; English.
                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU39992 standard; Protein; 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107077.
97FR-0015041.
97FR-0016034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.3%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                            98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 81.3
Best Local Similarity 81.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes.
                                                                                                                                                                                                                                                             WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200181581-A2.
                                                                                                                                                                        (GEST ) GENSET
                                                                                  04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-2000;
07-JUL-2000;
                                          27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
10-JUN-1999
                                                                                                                                                                                                                Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU39992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU39992
```

ö 셤

```
ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used in vaccinating them white ace used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them white aced to produce hosts cells which express the polypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH55971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynuclecide sequences from the present invention. AAH55091 to AAH55091 represent cligonuclecide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynuclecide sequences given in the sequence listing of the present specification, however the sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel elongation factors of Staphylococcus aureus useful as antibiotics for treating microbial diseases and infections, comprise a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB 22; Length 310;
Pred. No. 1.4e-07;
Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EF-Tu; elongation factor; antibiotic; anti-microbial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus elongation factor Tu.
                                                       18; Page 374; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96769 standard; Protein; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 36-37; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 kekfdrskehanigtighvdh 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US29098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0218197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Horn S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-442640/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA51329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200037495-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kallender H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY96769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The programmes on be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen
This is the Staphylococcus aureus elongation factor Tu (EF-Tu). EF-Tu is useful for treating an individual in need of enhanced activity or expression of EF-Tu. EF-Tu is useful as an antibiotic for treating microbial infections and diseases. An antagonist to EF-Tu is useful for treating an individual in need of inhibiting the activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr GJ;
                                                                                                                                                                                             Gaps
                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick JD,
                                                                                                                                                              Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                               Score 97; DB 21; Lengtn Jo-
Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus cellular proliferation protein #354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq ID No 5574; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL, Zyskind JW,
Xu HH;
                                                                                                                                                                                                                                                                                                                                      AAU34078 standard; Protein; 394 AA.
                                                                                                                                                                                          7
                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                            3 kekfdrskehanigtighvdh 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                            78.9%;
ilarity 81.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-611495/70.
                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                             394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS51937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2000;
22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3;
                                                                                                                                                                                                                                                                                                                                                                    AAU34078;
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                        33
                                                                                                                                                                                                                                                                                                                    AAU34078
                                                                                                                                                                                                                                                                                                                                                                      8888888888
                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                        q
```

```
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                              17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1999;
04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1999,
23-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4-MAY-1999
                                                                                                                                                                                                                                                                                        AAG12253;
                                                                                                        Sequence
                                                                                                                                         Query Match
                                                                                                                                                                                                                                             35
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                         AAG12253
                                                                                                                                                                                                                                             RESULT
                                                                                                                                                     Best
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                        888888888888
                                                                                                                                                                                       ŏ
                                                                                                                                                  ö
 proliferation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr GJ;
         a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
Xu HH;
                                                                                                                          Score 97; DB 22; Length 394;
Pred. No. 1.9e-07;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation protein #1019.
 for homologous nucleic acids which are required for cell
                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Seq ID No 12442; 511pp; English.
                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                     AAU36849 standard; Protein; 394 AA
                                                                                                                                                  ;
                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                    78.9%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-206848P.
2000US-207727P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191078P
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-269308P
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                         Ouery Match 78.99
Best Local Similarity 81.09
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611495/70.
                                                                                          394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS54708
                                                                                                                                                                                                                                                                                                                                                                                                      WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto RT,
                                                                                                                                                                                                                                                                                                  14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                            AAU36849;
                                                                                           Sequence
                                                                                                                                                                                                                                          AAU36849
                                                                                                                                                                                                                                                                           888888888888
                                                                                                                                                                         δ
                                                                                                                                                                                               g
```

```
ö
                               proliferation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                        Gaps
programmes. The antisense nucleic acid sequence is also useful to ifor homologous nucleic acids which are required for cell proliferal a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WHPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                       78.9%; Score 97; DB 22; Length 394; 81.0%; Pred. No. 1.9e-07; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays protein fragment SEQ ID NO: 11293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG12253 standard; Protein; 77 AA.
                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0123548.
99US-0125788.
99US-0126264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0130510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0131449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0132048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132486.
99US-0132487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0134218
99US-0134219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0126785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0132485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0132863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0134256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0134370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0134941
99US-0135124
                                                                                                                                                                                                                                                                                                                                                                                                              3 kekfdrskehanigtighvdh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0128234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0130891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0132407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0134768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                               Local Similarity 81.0 nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays subsp. mays
```

99018 - 0146388 99018 - 0146388 99018 - 0147301 99018 - 0147302 99018 - 0147302 99018 - 0147302 99018 - 0147303 99018 - 0147303 99018 - 0147493 99018 - 0147493 99018 - 0148841 99018 - 0148841 99018 - 0148841 99018 - 0148841 99018 - 0149126 99018 - 0151086 99018 - 0159284 99018 - 0159284 99018 - 0159284 99018 - 0159284 99018 - 0159284 99018 - 0160914 99018 - 0160914	99US-0161406. 99US-0161359. 99US-0161360. 99US-0161361.
02-AuG-1999; 03-AuG-1999; 04-AuG-1999; 04-AuG-1999; 05-AuG-1999; 05-AuG-1999; 06-AuG-1999; 06-AuG-1999; 06-AuG-1999; 06-AuG-1999; 11-AuG-1999; 12-AuG-1999; 13-AuG-1999; 13-AuG-1999; 13-AuG-1999; 14-AuG-1999; 15-SEP-1999; 16-SEP-1999; 17-AuG-1999; 18-AuG-1999; 19-AuG-1999; 11-AuG-1999; 11-AuG-1999; 12-AuG-1999; 13-AuG-1999; 13-AuG-1999; 14-AuG-1999; 14-AuG-1999; 15-SEP-1999; 16-AuG-1999; 17-AuG-1999; 18-AuG-1999; 18-AuG-1999; 19-SEP-1999; 19-SEP-1999; 11-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 14-CCT-1999; 13-CCT-1999; 14-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 13-CCT-1999; 14-CCT-1999; 15-CCT-1999; 15-CCT-1999; 16-CCT-1999; 17-CCT-1999; 18	
4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	PR P P P P P P P P P P P P P P P P P P
•	
99005-0135353. 99005-0135253. 99005-0136021. 99005-0136021. 99005-0136022. 99005-0137222. 99005-0137222. 99005-0137724. 99005-0137724. 99005-0139453. 99005-0139455. 99005-0139455. 99005-0139456. 99005-0139457. 99005-0139457. 99005-0139461. 99005-0139461. 99005-0139461. 99005-0139461. 99005-0139461. 99005-0139461. 99005-0139461. 99005-014287. 99005-014287. 99005-014287. 99005-014287. 99005-0144085. 99005-0144133. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-0144332. 99005-01445086. 99005-01445087.	S-014 S-014 S-014 S-014
21-MAY - 1999; 24-MAY - 1999; 25-MAY - 1999; 26-MAY - 1999; 26-MAY - 1999; 27-MAY - 1999; 28-MAY - 1999; 38-JUN	-JUL-19 -JUL-19 -JUL-19 -AUG-19

```
990S - 0137724
990S - 0138094
990S - 0138847
990S - 0139452
990S - 0139452
990S - 0139452
990S - 0139455
990S - 0139455
990S - 0139456
990S - 0139456
990S - 0139456
990S - 0139460
990S - 0139460
                                                                                                                                                                                                                                                                                                           99US-0139463.
99US-0139750.
99US-0139763.
99US-0139817.
99US-0140353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0144334.
990S-0144335.
990S-0144632.
990S-0144632.
990S-0144814.
990S-0145086.
990S-0145088.
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0140354.
99US-0140695.
99US-0140823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0140991.
99US-0141287.
99US-0141842.
99US-0142154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0142055.
99US-0142390.
99US-0142803.
99US-0142920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0144005.
99US-0144085.
99US-0144086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145192.
99US-0145145.
99US-0145218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0145919.
99US-0145951.
99US-0146386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0142977.
99US-0143542.
99US-0143624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144331.
99US-0144332.
99US-0144333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145224.
99US-0145276.
99US-0145913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0147204.
99US-0147302.
99US-0147192.
99US-0147260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0144325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0145089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0145918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0147038
04 - 70N - 1999

07 - 70N - 1999

10 - 70N - 1999

110 - 70N - 1999

111 - 70N - 1999

112 - 70N - 1999

113 - 70N - 1999

114 - 70N - 1999

115 - 70N - 1999

116 - 70N - 1999

117 - 70N - 1999

118 - 70N - 1999

119 - 70N - 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2 JUL - 1999

0.6 - JUL - 1999

0.7 JUL - 1999

1.2 - JUL - 1999

1.3 - JUL - 1999

1.4 - JUL - 1999

1.5 - JUL - 1999

1.6 - JUL - 1999

1.9 - JUL - 1999

2.0 - JUL - 1999

2.0 - JUL - 1999

2.1 - JUL - 1999

2.1 - JUL - 1999

2.2 - JUL - 1999

2.1 - JUL - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-1999;
27-JUL-1999;
28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1999
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                        Gaps
                                                                                                                        ;
0
                                                                                  Score 96; DB 21; Length 77;
Pred. No. 4.5e-08;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 11292.
                                                                                                                                                                                                                                                                        AAG12252 standard; Protein; 86 AA.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990S-0121825.
990S-0123180.
990S-01235180.
990S-0125788.
990S-01267854.
990S-0127462.
990S-0127462.
990S-0128714.
990S-0129845.
990S-013049.
990S-013048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0132486.
99US-0132487.
99US-0132863.
99US-0134256.
99US-0134218.
99US-0134211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0134370.
990S-0134768.
990S-0134341.
990S-0135124.
990S-0135629.
990S-013629.
990S-013629.
990S-013632.
990S-0137222.
                                                                                  Query Match 78.0%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-0301439
                                                                                                                                                     17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays subsp. mays
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-1999;
19-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MAY 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MAY-1999;
-MAY-1999;
-MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -JUN-1999;
-JUN-1999;
-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000
                                                                                                                                                                                                                                                                                                             AAG12252;
                                                                                                                                                                                                                                            RESULT 36
                                                                                                                                                                                                                                                              AAG12252
 PR
PR
PR
                                                                                                                                                         à
                                                                                                                                                                                       윰
```

```
25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

08-APR-1999

119-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

26-APR-1999

26-APR-1999

27-APR-1999

28-APR-1999

28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 - MAY - 1999;
28 - MAY - 1999;
01 - JUN - 1999;
03 - JUN - 1999;
04 - JUN - 1999;
07 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                          AAG12476;
           Matches
                                                                                                                                                                                                           RESULT 3
                                                                                                                    g
                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 96; DB 21; Length 86; Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.0%;
88.9%;
  990S - 0147303 - 990S - 0147416 - 990S - 0147416 - 990S - 0147416 - 990S - 0147416 - 990S - 0147935 - 990S - 0148317 - 990S - 0148311 - 990S - 0149328 - 990S - 0149329 - 990S - 0159330 - 990S -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AuG-1999

11-SEP-1999

13-SEP-1999

13-SEP-1999

14-SEP-1999

15-SEP-1999

16-SEP-1999

16-SEP-1999

17-SEP-1999

18-SEP-1999

19-SEP-1999

19-SEP-1999

19-SEP-1999

11-OCT-1999

11-OC
06-AUG-1999,
06-AUG-1999,
09-AUG-1999,
110-AUG-1999,
113-AUG-1999,
113-AUG-1999,
113-AUG-1999,
113-AUG-1999,
113-AUG-1999,
114-AUG-1999,
20-AUG-1999,
20-AUG-1999,
21-AUG-1999,
22-AUG-1999,
23-AUG-1999,
23-AUG-1999,
23-AUG-1999,
23-AUG-1999,
23-AUG-1999,
23-AUG-1999,
23-AUG-1999,
27-AUG-1999,
27-AUG-1999,
```

ö Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn. Gaps ö Indels ;; Zea mays protein fragment SEQ ID NO: 11603. Mismatches AAG12476 standard; Protein; 111 AA. 1; 990S-0121825 990S-012358 990S-012358 990S-0125788 990S-0126785 990S-0126785 990S-0127465 990S-0127465 990S-0129845 990S-0130077 990S-0130891 990S-0130891 990S-0132486 990S-0132486 990S-0132486 990S-0132486 990S-0134286 990S-0134286 990S-0134286 990S-0134286 990S-0134218 99US-0137724 99US-0138094 99US-0138540 99US-0138847 99US-0139119 99US-0139452 25-FEB-2000; 2000EP-0301439 5 FNRTKPHVNIGTIGHVDH 22 17-OCT-2000 (first entry) 16; Conservative Zea mays subsp. mays 10-JUN-1999; 10-JUN-1999; 14-JUN-1999; 16-JUN-1999;

90S - 0139453 90S - 0139455 90S - 0139455 90S - 0139456 90S - 0139456 90S - 0139450 90S - 0139461 90S - 0139461 90S - 0139461 90S - 0139463 90S - 0139463 90S - 0139463 90S - 0139763 90S - 0139763	905.0140695 905.0140695 905.0140695 905.0140829 905.0141287 905.0142390 905.0142390 905.0142390 905.014332 905.0144332 905.0144333 905.0144333 905.0144333 905.0144333 905.0144333	ά ά ά ά ά ά α α ά α α ά α α α α α α α α
2-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999 8-700-1999	8 - 700 - 1399 8 - 700 - 1399 9 - 100 - 1399 9 - 100 - 1399 10 - 100 - 1399 11 - 100 - 1399 12 - 100 - 1399 13 - 100 - 1399 14 - 100 - 1399 15 - 100 - 1399 16 - 100 - 1399 17 - 100 - 1399 18 - 100 - 1399 19 - 100 - 1399 10 - 100 - 100 - 1399 10 - 100 - 100 - 1399 10 - 100 - 100	AUG AUG AUG AUG AUG AUG AUG AUG AUG AUG
	*	

		; ;	
			8e-08; s 1;
			O
014936 014942 014942 014972 014992 014990	0015056 0015088 0015100 0015100 00151308 00151303 00152303 00152303 00152303 00152303 0015513 0015513 0015513 0015513	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	88.9%; vative SHVDH 22
			Similar 5; Cor FKPHVN
-AUG -AUG -AUG -AUG -AUG	25-AUG 27-AUG 27-AUG 27-AUG 30-AUG 31	PR PR 96 - 00 - 00 - 00 - 00 - 00 - 00 - 00 -	Best Local S Matches 16 Oy 5 FNR

0;

us-09-488-737-1.rag

```
990S-0139459-990S-0139460-990S-0139461-990S-0139462-990S-0139753-990S-0139753-990S-0140353-990S-0140359-990S-0142395-990S-0142395-990S-0142390-990S-0142390-990S-0142390-990S-0142390-990S-0142390-990S-0142390-990S-0142390
                                                                                                                                                                                                                                                                                                                                                                                                  990S-0143542.
990S-0144005-
990S-0144085.
990S-0144086.
990S-0144325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0145089.
99US-0145192.
99US-0145218.
99US-0145218.
99US-0145276.
99US-0145276.
99US-0145913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  990S - 0145951
990S - 0146386
990S - 0146389
990S - 0146389
990S - 0147303
990S - 0147302
990S - 0147302
990S - 0147303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0144352.
990S-0144352.
990S-0144632.
990S-0144884.
990S-0144814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0148565.
99US-0148684.
99US-0149368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0144332.
99US-0144333.
99US-0144334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0149175.
99US-0149426.
99US-0149722.
99US-0149723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0145088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0145085
99US-0145087
18 - JUN - 1999;

23 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

25 - JUN - 1999;

26 - JUN - 1999;

27 - JUL - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUL - 1999;

20 - JUL - 1999;

21 - JUL - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

25 - JUN - 1999;

26 - JUN - 1999;

27 - JUL - 1999;

28 - JUN - 1999;

29 - JUL - 1999;

20 - JUL - 1999;

21 - JUL - 1999;

21 - JUL - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

25 - JUN - 1999;

26 - JUN - 1999;

27 - JUN - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUN - 1999;

21 - JUN - 1999;

21 - JUN - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

25 - JUN - 1999;

26 - JUN - 1999;

27 - JUN - 1999;

28 - JUN - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUN - 1999;

21 - JUN - 1999;

22 - JUN - 1999;

23 - JUN - 1999;

24 - JUN - 1999;

25 - JUN - 1999;

26 - JUN - 1999;

27 - JUN - 1999;

28 - JUN - 1999;

28 - JUN - 1999;

28 - JUN - 1999;

29 - JUN - 1999;

20 - JUN - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 - JUL - 1999

02 - AUG - 1999

02 - AUG - 1999

03 - AUG - 1999

04 - AUG - 1999

05 - AUG - 1999

06 - AUG - 1999

06 - AUG - 1999

10 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

17 - AUG - 1999

18 - AUG - 1999

19 - AUG - 1999

10 - AUG - 1999

11 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

16 - AUG - 1999

17 - AUG - 1999

18 - AUG - 1999

19 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999

11 - AUG - 1999

11 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

16 - AUG - 1999

17 - AUG - 1999

18 - AUG - 1999

18 - AUG - 1999

19 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

16 - AUG - 1999

17 - AUG - 1999

18 - AUG - 1999

18 - AUG - 1999

18 - AUG - 1999

19 - AUG - 1999

19 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

16 - AUG - 1999

17 - AUG - 1999

18 - A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-1
                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                            Zea mays protein fragment SEQ ID NO: 11601
                                    AAG12474 standard; Protein; 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S - 0.138540.
990S - 0.138847.
990S - 0.1394119.
990S - 0.139453.
990S - 0.139454.
990S - 0.139455.
990S - 0.139456.
                                                                                                                                                                                                                                                                                                                                                                                                99US-0121825.
99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
99US-0127462.
99US-0128714.
99US-0128714.
99US-012814.
99US-013845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0130891
9905-0131449
9905-0132407
9905-0132487
9905-0132487
9905-0132487
9905-0132487
9905-0132487
9905-013428
9905-013428
9905-013428
9905-013428
9905-0134219
9905-0134318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0136021.
99US-0136392.
99US-0136782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0137528
99US-0137502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0137724
99US-0138094
                                                                                                                                                                                                                                                                                                                                                                 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0135629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0137222
                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                         Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                              04 - JUN - 1999;
07 - JUN - 1999;
08 - JUN - 1999;
10 - JUN - 1999;
14 - JUN - 1999;
16 - JUN - 1999;
16 - JUN - 1999;
17 - JUN - 1999;
18 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                         EP1033405-A2
                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                        AAG12474;
RESULT 38
AAG12474
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                   Zea mays protein fragment SEQ ID NO: 55934.
                                                                                                                                                                                                                                990S-0121825.
990S-0123180.
990S-0123548.
990S-0125788.
990S-0126264.
                                                                                                                                                                                                                                                                                                                          9905-0127462
9905-0127462
9905-0128714
9905-0128714
9905-0129454
9905-0130401
9905-0130401
9905-0130401
9905-0132485
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0132486
9905-0134218
9905-0134218
9905-0134218
9905-0134218
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
9905-013629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139458.
99US-0139459.
99US-0139460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0139461.
990S-0139462.
990S-0139463.
990S-0139750.
                                                                                                                                                                                                       2000EP-0301439
                                                                                                             Zea mays subsp. mays
                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                     25-FEB-2000;
                                                                                                                                                                                                                                25-FEB-1999;
05-MAR-1999;
03-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
13-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 - MAY - 1999;
18 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1999;
                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; DB 21; Length 129;
Pred. No. 8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG44634 standard; Protein; 156 AA.
                                            990S-0150566
990S-0150884.
990S-0151065.
990S-0151066.
990S-0151303.
 99US-0149929.
99US-0149902.
99US-0149930.
                                                                                                                                                     990S-0151930.
990S-0152363.
990S-0153070.
990S-0153758.
                                                                                                                                                                                                                  99US-0154018.
99US-0154039.
99US-0154779.
                                                                                                                                                                                                                                                             99US-0155139.
99US-0155486.
99US-0155659.
                                                                                                                                                                                                                                                                                                        990S-0156458.
990S-0156596.
990S-0157117.
990S-0157865.
990S-0158029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0158369.
990S-0159293.
990S-0159294.
990S-0159295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0159637.
99US-0159638.
99US-0159584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0160814.
990S-0160815.
990S-0160980.
990S-0160989.
990S-0161404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-016140S-
990S-0161406-
990S-0161369-
990S-0161369-
990S-0161361-
990S-0161920-
990S-0161932-
990S-0161933-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0160741.
99US-0160767.
99US-0160768.
99US-0160770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0159329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0159330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 FNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ftrtkphynygtighydh 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 88.9
les 16; Conservative
20 - AUG - 1999;
23 - AUG - 1999;
25 - AUG - 1999;
26 - AUG - 1999;
27 - AUG - 1999;
27 - AUG - 1999;
30 - AUG - 1999;
10 - SEP - 1999;
113 - SEP - 1999;
115 - SEP - 1999;
12 - SEP - 1999;
22 - SEP - 1999;
23 - SEP - 1999;
24 - SEP - 1999;
24 - SEP - 1999;
                                                                                                                                                                                                                                                                                                        28 - SEP - 1999

29 - SEP - 1999

05 - OCT - 1999

07 - OCT - 1999

13 - OCT - 1999

13 - OCT - 1999

14 - OCT - 1999

16 - OCT - 1999

17 - OCT - 1999

18 - OCT - 1999

18 - OCT - 1999

18 - OCT - 1999

19 - OCT - 1999

21 - O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
25.0CT-1999
25.0CT-1999
26.0CT-1999
26.0CT-1999
26.0CT-1999
28.0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG44634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
```

AAG44634 ID AAG4 XX AC AAG4 XX DT 18-0

ò ΩD

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0147260.
990S-0147303.
990S-0147416.
990S-0147493.
990S-0147935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990S-0149930.
990S-0150566.
990S-0150884.
990S-0151065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S - 0145145
990S - 0145218
990S - 0145274
990S - 0145274
990S - 0145918
990S - 0145918
990S - 0145918
990S - 0145918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0147038.
99US-0147204.
99US-0147302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0148341.
99US-0148565.
99US-0148684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0149368.
99US-0149175.
99US-0149426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0149723.
99US-0149929.
99US-0149902.
             990S-0139899
990S-0140353
990S-0140354
990S-01406923
990S-0141287
990S-0141287
990S-0141287
990S-0142055
990S-0142055
990S-0142055
990S-0142920
990S-0142920
990S-0143542
990S-0144085
990S-0144085
990S-0144085
                                                                                                                                                                                                                                                                                                                               99US-0144335.
99US-0144352.
99US-0144632.
99US-0144884.
                                                                                                                                                                                                                                                                                                                                                                                  99US-0144814.
99US-0145086.
99US-0145088.
                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0145085.
990S-0145087.
99US-0145089.
99US-0145192.
                                                                                                                                                                                                                                                                           99US-0144331.
99US-0144332.
99US-0144333.
99US-0144334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0146389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0147192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0148319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0149722
    99US-0139817
21 - JUN - 1999;
23 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
26 - JUN - 1999;
27 - JUN - 1999;
28 - JUN - 1999;
30 - JUL - 1999;
30 - JUL - 1999;
31 - JUL - 1999;
31 - JUL - 1999;
32 - JUL - 1999;
33 - JUL - 1999;
34 - JUL - 1999;
35 - JUL - 1999;
36 - JUL - 1999;
37 - JUL - 1999;
38 - JUL - 1999;
39 - JUL - 1999;
30 - JUL - 1999;
31 - JUL - 1999;
31 - JUL - 1999;
32 - JUL - 1999;
31 - JUL - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                      22 - 70L - 1999
22 - 70L - 1999
23 - 70L - 1999
23 - 70L - 1999
23 - 70L - 1999
24 - 70L - 1999
25 - 70L - 1999
26 - 70L - 1999
27 - 70L - 1999
27 - 70L - 1999
28 - 70L - 1999
28 - 70L - 1999
29 - 70L - 1999
20 - 80C -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11. AUG-1999
12. AUG-1999
13. AUG-1999
13. AUG-1999
16. AUG-1999
17. AUG-1999
20. AUG-1999
23. AUG-1999
23. AUG-1999
25. AUG-1999
25. AUG-1999
27. AUG-1999
```

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn. Gaps ö Length 156; Score 96; DB 21; Length 15 Pred. No. 9.8e-08; Zea mays protein fragment SEQ ID NO: 55933. 1; Mismatches AAG44633 standard; Protein; 175 AA 990S-0151080 990S-0151303 990S-0151303 990S-0151303 990S-015363 990S-015363 990S-0153780 990S-0154039 990S-0154039 990S-0155639 990S-0156458 990S-0156458 990S-0156458 990S-0156458 990S-0156459 990S-015929 990S-015929 990S-0159330 990S-0159331 78.0%; 88.9%; 990S-0159584 990S-0159584 990S-0160767 990S-0160770 990S-0160814 990S-0160814 990S-0160980 990S-0160980 990S-0161406 990S-0161406 990S-0161359 990S-0161359 990S-01613360 990S-01613360 990S-01613360 990S-01613360 18-OCT-2000 (first entry) 5 FNRTKPHVNIGTIGHVDH 22 Best_Local Similarity 88.9 Matches 16; Conservative 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 10-SEP-1999; 110-SEP-1999; 110-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 24-OCT-1999; 24-18 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 22 - OCT - 1999 25 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 28 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 AAG44633; Query Match 40 9 RESULT 4 AAG44633

99US-0141842. 99US-0142154. 99US-0142055.	99US-0142390. 99US-0142803. 99US-0142920.	99US-0142977. 99US-0143542. 99US-0143624.	99US-0144005.	99US-0144086.	990S-0144325. 990S-0144331.	99US-0144332.	99US-U144333. 99US-0144334.	99US-0144335.	990S-0144632.	99US-0144884.	99US-0145086.	990S-0145088. 990S-0145085.	99US-0145087.	990S-0145089. 990S-0145192.	99US-0145145.	990S-0145218. 990S-0145224.	99US-0145276.	99US-0145918.	99US-0145919. 99US-0145951.	99US-0146386.	99US-0146389.	99US-014/038. 99US-0147204.	99US-0147302.	990S-0147260.	990S-014/303.	99US-0147493. 99US-0147935.	99US-0148171.	99US-0148341.	99US-0148565.	99US-0149368.	99US-01491/5. 99US-0149426.	99US-0149722.	99US-0149929.	99US-0149902.	990S-0150566.	99US-0150884. 99US-0151065.	990s-0151066.	990S-0151080. 990S-0151303.	99US-0151438.	9908-0152363. 9908-0152363.	990S-0153758.
01-JUL-1999; 01-JUL-1999; 02-JUL-1999;	06-JUL-1999; 08-JUL-1999; 09-JUL-1999;	12-JUL-1999; 13-JUL-1999; 14-JUL-1999;	15-JUL-1999;	16-JUL-1999;	19-JUL-1999; 19-JUL-1999;	19-JUL-1999;	19-JUL-1999; 19-JUL-1999;	19-JUL-1999;	20-JUL-1999;	20-JUL-1999; 21-JUL-1999;	21-JUL-1999;	21-JUL-1999; 22-JUL-1999;	22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	23-JUL-1999;	23-JUL-1999; 23-JUL-1999;	26-JUL-1999; 27-JHL-1999;	27-JUL-1999;	27-JUL-1999; 28-JUL-1999;	02-AUG-1999;	02-AUG-1999;	03-AUG-1999; 04-AUG-1999;	04-AUG-1999; 05-AUG-1999;	05-AUG-1999;	06-AUG-1999;	09-AUG-1999; 09-AUG-1999;	10-AUG-1999;	12-AUG-1999;	13-AUG-1999; 13-AUG-1999;	16-AUG-1999;	1/-AUG-1999; 18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	25-AUG-1999;	26-AUG-1999; 27-AUG-1999;	27-AUG-1999;	27-AUG-1999; 30-AUG-1999;	31-AUG-1999;	07-SEF-1999; 07-SEP-1999; 10-SEP-1999.	13-SEP-1999;
PR PR																																									
									•																																
								٠					•							•														•					•		
	2000EP-0301439	99US-0121825. 99US-0123180.	99US-0123548 99US-0125788	99US-0126264	99US-0127462	99US-0128234	99US-0129845	99US-0130077	990S-0130510	99US-0130891 99US-0131449	99US-0132048	99US-U13248V	99US-0132485	99US-0132487	99US-0132863	990S-0134218	99US-0134219 99US-0134221	99US-0134370	99US-U134/68 99US-0134941	99US-0135124 99US-0135353	990s-0135629	990S-0136392	99US-0136782 99US-0137222	990S-0137528	99US-0137724	99US-0138094 99US-0138540	99US-0138847	990S-0139452	99US-0139453 99US-0139492	99US-0139454	990S-0139456	99US-0139457 99US-0139458	99US-0139459	99US-0139460 99US-0139461	990S-0139462	990S-0139463 990S-0139750	99US-0139763	990S-0139817	99US-0140353 99US-0140354	990S-0140695	09015-0140991
EP1033405-A2.	5-FEB-2000;	25-FEB-1999; 05-MAR-1999;	666	666	999	666	999	999	999	5 5 5 5 5	666	999	999	999	999	966	666 666	666	666	666 666	666	999	666 666	999	999	999	666	999	999	999	999	666	666	666	666	999	666	900	6666	24 - JUN-1999; 28 - JUN-1999;	000
XXX																																									

```
PR 15-SEP-1999 99US-0154018.

PR 20-SEP-1999 99US-0154018.

PR 22-SEP-1999 99US-0155659.

PR 22-SEP-1999 99US-0155659.

PR 22-SEP-1999 99US-0155659.

PR 23-SEP-1999 99US-0155659.

PR 24-SEP-1999 99US-0155659.

PR 04-CCT-1999 99US-015659.

PR 06-CCT-1999 99US-0157117.

PR 06-CCT-1999 99US-015765.

PR 11-CCT-1999 99US-015869.

PR 11-CCT-1999 99US-015869.

PR 11-CCT-1999 99US-0158769.

PR 21-CCT-1999 99US-0158769.

PR 21-CCT-1999 99US-016876.

PR 21-CCT-1999 99US-016091.

PR 21-CCT-1999 99US-016091.

PR 21-CCT-1999 99US-016091.

PR 22-CCT-1999 99US-016091.

PR 23-CCT-1999 99US-016091.

PR 23-CCT-1999 99US-016091.

PR 23-CCT-1999 99US-016091.

PR 23-CCT-1999 99US-016092.

PR 23-CCT-1999 99US-016093.

PR 23-CCT-1999 99US-016093.
```

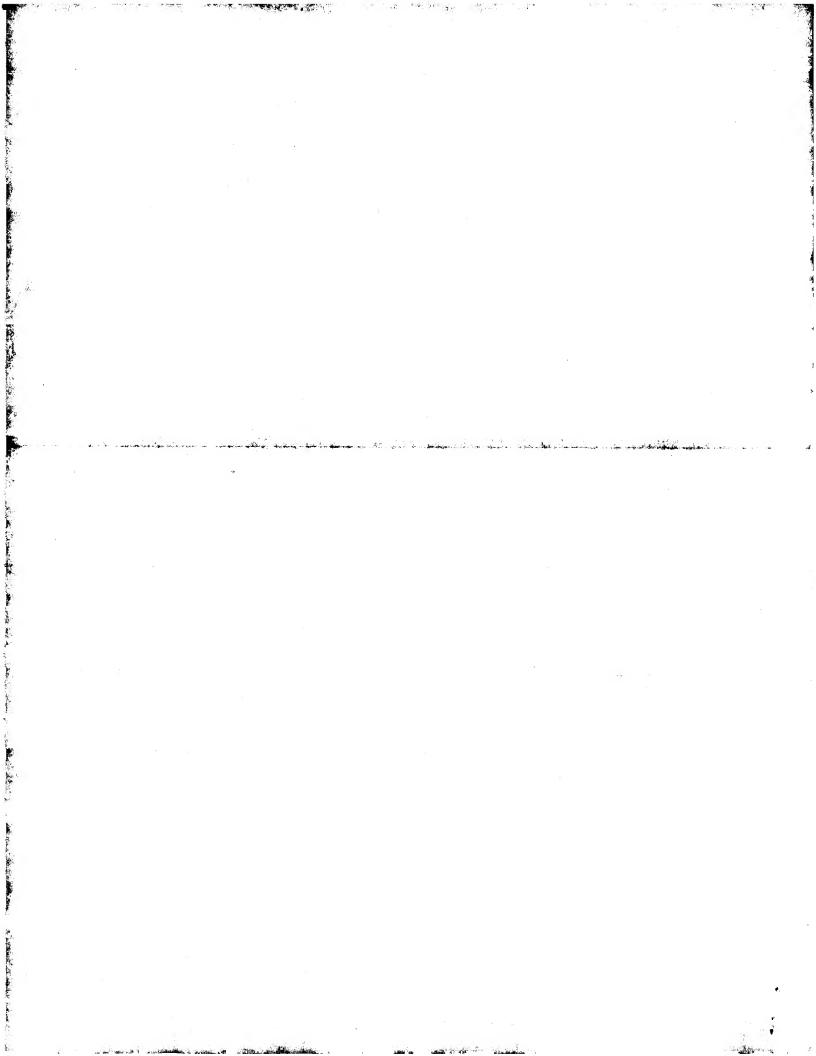
ö

Gaps

ö

Query Match 78.0%; Score 96; DB 21; Length 175; Best Local Similarity 88.9%; Pred. No. 1.1e-07; Matches 16; Conservative 1; Mismatches 1; Indels

Search completed: August 22, 2002, 07:44:04 Job time: 63 sec



```
herpetosiph
aquifex aeo
aquifex pyr
chlorella v
agrobacteri
guillardia
                                                                                                                                                                                                                                                  chara conni
codium frag
ciknenla c
chlamydia m
chlamydia p
chlamydia t
cytophaga 1
flavobacter
shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                      astasia lon
cyclotella
synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        porphyra pu
spirulina p
treponema p
bacillus ha
bacillus su
thermus aqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycine max
glycine max
mycoplasma
                                                                                                                                                                                                 mesostigma
borrelia bu
brevibacter
chara conni
                                                                                                                                                                                                                                                                                                                                                                                                     flexistipes
deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           planobispor
arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synechocyst
wolinella s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pisum sativ
spirochaeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          micrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deinonema s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               xylella fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  schizosacch
fervidobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treponema h
                                  mycoplasma
burkholderi
                                                                helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synechococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chlamydomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nicotiana t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermoplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apple proli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chlorobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyrococcus
               P13927 III 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                EFTU_HERAU
EFTU_AQUAE
EFTU_AQUPY
                                                                                                                                                                                                                                                  EFTU_CHACO
EFTU_CODFR
EFTU_EIKCO
                                                                                                                                                                                                                                                                                                                     EFTU_CHLPN
EFTU_CHLTR
EFTU_CYTLY
EFTU_FLAFE
EFTU_SHEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                        EFTU_ASTLO
EFTU_CYCME
EFTU_SYNP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_BACHD
EFTU_BACSU
EFTU_THEAQ
EFTU_THETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFTU_CHLRE
EFTU_PLARO
EFTU_ARATH
                                                                                                                                                                                                                   EFTU_BORBU
EFTU_BRELN
                                                                                                                                                                                                                                                                                                 EFTU_CHLMU
EFTU_CHLPN
EFTU_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_FLESI
EFTU_DEIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTU_DEISP
EFTU_PORPU
EFTU_SPIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_YEAST
EFTU_PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTU_FERIS
EFTU_APPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF1A_PYRAB
EF1A_PYRHO
                                                EFTU_BURCE
EFTU_HELPJ
                                                                                                                                                  EFTU_CHLVU
EFTU_AGRTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFT1_SOYBN EFT2_SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFTU_WOLSU
EFTU_CYAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFTU_CHLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_MYCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_XYLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_SPIAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFT3_STRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF1A_PYRWO
                                                                                                                                                                                   SFTU_GUITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFTU_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFTU_TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFTU_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFTU_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFTU_TREHY
                                                                                                                                                                                                     SFTU_MESVI
\frac{1}{2} \frac{1}
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pasteurella
pasteurella
odontella s
nephroselmi
campylobact
neisseria g
reclinomona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stigmatella
thermotoga
rickettsia
ureaplasma
bacillus st
corynebacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   streptomyce
streptomyce
streptomyce
streptomyce
euglena gra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteroides
escherichia
haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mycobacteri
thiobacillu
                                                                                                              Search time 13.53 Seconds (without alignments) 62.959 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P56003 helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    streptococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhizobium l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43926
P21694
P21694
P57939
P57939
P57936
P4822
P4823
P42445
P42445
P42445
P42445
P50865
P508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P95724
P33170
P82559
Q981f7
P18906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q53871
P29542
P29543
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                 105224 segs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_HELPY
EFTU_BACER
EFTU_HAEIN
EFTU_HAEIN
EFTU_HAEIN
EFTU_HAEIN
EFTU_NEE
EFTU_NEC

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFT1_STRRA
EFT2_STRRA
EFT0_STRAU
EFT0_EUGGR
                                                                                - protein search, using sw model
                                                                                                               August 22, 2002, 07:43:01
                                                                                                                                                                                                     123
1 MKEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                   US-09-488-737-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of
                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                     Sequence:
                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
```

EFTU_HELPY

```
C -1 - SUBGULTA MONOMER (BY SIMILARITY).

-1 - SUBJULTARITY DOCATION: Cytoplasmic.
-1 - SUBJULARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

R INTERPOSED SUBFAMILY.

R PÉTAN, PRO00095; GTP_EFTU_D2.

R PÉTAN, PRO00099; GTP_EFTU_D2.

R PÉTAN, PRO13144; GTP_EFTU_D2; 1.

R PÉTAN, PRO13145; GTP_EFTU_D2; 1.

R PRINTS; PRO0315; ELONGATNECT.

R PRINTS; PRO0315; ELONGATNECT.

R PROSITE; PRO0301; EFACTOR_GTP; 1.

R PRINTS; PRO0315; GTP_EFTU_D3; 1.

R PRINTS; PRO0315; ELONGATNECT.

R PROSITE; PRO0301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROW N.A.

MEDLINES-90240875; PubMed=2110445;

Ludwig W., Weizenegger M., Betzl D., Leidel E., Lenz T., Ludvigsen A.,

Moellenhoff D., Wenzig P., Schleifer K.H.;

"Complete nucleotide sequences of seven eubacterial genes coding for
the elongation factor Tu: functional, structural and phylogenetic
evaluations.";
                                                                                                                                                                                                       Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arch. Microbiol. 153:241-247(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (TUFB).
MEDLINE-81165558; PubMed=7011904;
MRD./INE-81165558; DubMed=7011904;
MRD G., Friesen J.D.;
"The nucleotide sequence of tufB and four nearby tRNA structural genes of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112; DB 1; Length 39
Pred. No. 5.9e-11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
7B4C6FD208323149 CRC64;
                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71-JUL-1986 (Rel. 01, Created)
01-MRR-1989 (Rel. 10, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
16-ngation factor Tu (EF-Tu) (P-43)
(TUFA OR B3339) AND (TUFB OR B3980).
   394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 139 C
394 AA; 43580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.18; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KEKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 91.1
Best Local Similarity 95.2
Matches 20; Conservative
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                            NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTU_ECOLI
P02990;
   EFTU_BACFR
P33165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
EFTU_ECOLI
         HDD DD BRAND DD BRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97394467; PubMed=9252185;
MEDLINE-97394467; PubMed=9252185;
MEDLINE-97394467; PubMed=9252185;
MEDLINE-97394467; PubMed=9252185;
Melson R.D. Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Mitterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori (Campylobacter pylori).
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
MW; 502751637BDA2707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03145; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB 1; I
Pred. No. 6.1e-12;
                                                (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.9%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000626; AAD08250.1; -.
                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sec
16-OCT-2001 (Rel. 40, Last and
Elengation factor Tu (EF-Tu).
TUF OR TUFA OR HP1205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 1
399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HP1205;
                                                                                                                                                                                                                                                          Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Loral Simi
Matches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
NP_BIND
SEQUENCE
```

pylori.

ö

Gaps

; 0

NP_BIND

2

RESULT

g ò

Length 394;

```
Bosch L.
    Laursen R.A., L'Italien J.J., Nagarkatti S., Miller D.L.; "The amino acid sequence of elongation factor Tu of Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     properties of proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-82124558; PubMed-7035813;
Miyajima A., Shibuya M., Kuchino Y., Kaziro Y.;
Miranscription of the E. coli tufB gene: cotranscription with four
tRNA genes and inhibition by
guanosine-5'-diphosphate-3'-diphosphate.";
                                                                                                                               Daniels D.L.;
"Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes.";
Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND 382-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lippmann C., Lindschau C., Vijgenboom E., Schroeder W., Bosch L., Erdmann V.A.;
                                                                                                                                                                                                                             SEQUENCE FROM N.A. (TUFA).
MEDLINE-81165557; PubMed-7011903;
YOKOTA T., Sugisaki H., Takanami M., Kaziro Y.;
"The nucleotide sequence of the cloned tufA gene of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones M.D., Petersen T.E., Nielsen K.M., Magnusson S., Sottrup-Jensen L., Gausing K., Clark B.F.C.; "The complete amino-acid sequence of elongation factor {\tt Tu} from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prokaryotic elongation factor Tu is phosphorylated in vivo.";
J. Biol. Chem. 268:601-607(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Young C.C., Bernlohr R.W.;
"Elongation factor Tu is methylated in response to nutrient deprivation in Escherichia coli.";
J. Bacteriol. 173:3096-3100(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                    Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITE THR-382, AND SEQUENCE OF 289-303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE OF 152-175 AND 261-289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed pi
in the genome of Escherichia coli K-12."
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 108:507-526(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete sequence.";
J. Biol. Chem. 256:8102-8109(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-20 FROM N.A. (TUFB).
                                     SEQUENCE FROM N.A. (TUFB).
STRAIN-K12 / MG1655;
MEDLINE-94089392; PubMed-8265357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91216980; PubMed=2022614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-81003875; PubMed-6997043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81264196; PubMed-7021545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97443975; PubMed-9298646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93107067; PubMed-8416965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-12 AND 310-321.
STRAIN-K12 / EMG2;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (TUFA).
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                    Gene 12:25-31(1980)
Sene 12:33-39(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                             Daniels D.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-B/R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                   coli.
$\text{1}$\text{2}\text{3}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\text{5}\tex
```

```
"The structural and functional basis for the kirromycin resistance of mutant EF-Tu species in Escherichia coli.";
EMBO J. 13:4877-4885(1994).
                                                                                                                                                                                                                                                                                                                      Effects on the and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-90216700; PubMed-2157708;
Cool R.H., Jensen M., Jonak J., Clark B.F.C., Parmeggiani A.;
"Substitution of proline 82 by threonine induces autophosphorylating
activity in GTP-binding domain of elongation factor Tu.";
J. Biol. Chem. 265:6744-6749(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang Y., Yu N.J., Spremulli L.L.;
"Mutestional analysis of the roles of residues in Escherichia coli
elongation factor Ts in the interaction with elongation factor Tu.";
J. Biol. Chem. 273:4556-4562(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97133305; PubMed-8978702; Vorstenbosch E., Pape T., Rodnina M.V., Kraal B., Wintermeyer W.; The G222D mutation in elongation factor Tu inhibits the codon induced conformational changes leading to GFPase activation on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS RESISTANT TO KIRROMYCIN.
MEDLINE-95045380; PubMed-7525272;
Mesters J.R., Zeef L.A.H., Hilgenfeld R., de Graaf J.M., Kraal B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hwang Y.-W., McCabe P.G., Innis M.A., Miller D.L.; "Site-directed mutagenesis of the GDP binding domain of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILNE-88007508; PubMed=3308869;
Hwang Y.-W., Miller D.L.;
Hwang Yint in that alters the nucleotide specificity of elongation
factor Tu, a Pre regulatory protein.";
J. Biol. Chem. 262:13081-13085(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ø
                                                               L'Italien J.J., Laursen R.A.; "Location of the site of methylation in elongation factor Tu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeef L.A.H., Bosch L., Anborgh P.H., Cetin R., Parmeggiani A., Hilgenfeld R.; "Pulvomycin-resistant mutants of E.coli elongation factor Tu."; EMBO J. 13:5113-5120(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hwang Y.-W., Sanchez A., Miller D.L.;
"Mutagenesis of bacterial elongation factor Tu at lysine 136.
conserved amino acid in GTP regulatory proteins.";
J. Biol. Chem. 264:8304-8309(1989).
                                                                                                                                                                                                                                                                                    Jacquet E., Parmeggiani A.; "Substitution of Val20 by Gly in elongation factor Tu. "Substitution with elongation factors Ts, aminoacyl-tRNA ribosomes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 75-89, AND MUTAGENESIS OF PRO-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS OF HIS-19; GLN-114 AND GLU-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch. Biochem. Biophys. 274:394-403(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION OF MUTANT ASP-222.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 185:341-346(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89255270; PubMed-2498311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90025117; PubMed-2508560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98136155; PubMed-9468511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS RESISTANT TO PULVOMYCIN.
MEDLINE-95045403; PubMed=7957075;
                                                                                                                                                                                                                                               MEDLINE=90060119; Pubmed=2684669;
                             MEDLINE-80069392; PubMed-389663;
                                                                                                                                      FEBS Lett. 107:359-362(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the ribosome.";
EMBO J. 15:6766-6774(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [15]
MUTAGENESIS OF LYS-136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF ASP-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  elongation factor Tu."
                                                                                                                                                                               [12]
MUTAGENESIS OF VAL-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS
METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                 ribosomes.
```

```
"Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137
            influenzae Rd.
                                                                                                                                                                                                                                                              HSSP; P02990;
TIGR; HI0578;
TIGR; HI0632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTU_SALTY P21694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND
NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
EFTU_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
  ö
                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: MAY PLAY AN IMPORTANT REGULATORY ROLE IN CELL GROWTH AND IN THE BACTERIAL RESPONSE TO NUTRIENT DEPRIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: CYTOPLASMIC, AND MEMBRANE-ASSOCIATED.
                       (jeldgaard M., Nyborg J.; Refined structure of elongation factor EF-Tu from Escherichia coli.";
                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
MEDLINE-99141376; PubMed-9918724;
Song H., Parsons M.R., Rowsell S., Leonard G., Phillips S.E.V.;
Crystal structure of intact elongation factor EF-Tu from Escherichia coli in GDP conformation at 2.05-A resolution.";
J. Mol. Biol. 285:1245-1256(1999).
- PUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMMONORYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                  Leberman R.;
                                                                                                                                                                        Kawashima T., Berthet-Colominas C., Wulff M., Cusack S., Leberman R.;
Nature 381:172-172(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIZINE—95550630; PubMed=7542800; Playton R.A., Kirkness E.F., Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.T., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                       X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH EF-TS.
MEMBLINE-S6170031; PubMed-8596629;
Kawashima T., Berribet-Colominas; C. Wulff M., Cusack S., Lek
"The structure of the Escherichia coli EF-Tu.EF-Ts complex a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 111; DB 1; Length 393;
Pred. No. 8.6e-11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                        MEDLINE-97094972; PubMed-8939740;
Abel K., Yoder M.D., Hilgenfeld R., Jurnak F.;
An alpha to beta conformational switch in EF-Tu.";
Structure 4:1153-1159(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
(TUFA OR HI0578) AND (TUFB OR HI0632).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 AA.
                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=92177415; PubMed=1542116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                 J. Mol. Biol. 223:721-742(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFERTKPHVNVGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.24
Best Local Similarity 90.55
Matches 19; Conservative
                                                                                                                                     Nature 379:511-518(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
                                                                                                                        resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_HAEIN
P43926;
                                                                                                                                                              ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTU_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                          BIOSYNTHESIS.
--- SUBGNIT: MONOMER (BY SIMILARITY).
--- SUBCELLUAR LOCATION: Cytoplasmic.
--- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSOCIATED WITH AMINOACYL-TRNA BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium; STRAIN-LT2;
MEDLINE-91002658; PubMed-2207156;
Tuohy T.M.F., Thompson S., Gesteland R.F., Hughes D., Atkins J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
ASSOCIATED WITH GUANOSINE NUCLEOTIDE
                         FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING ACTIVITIES (BY SIMILARITY). 2430107FD71A038C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhi.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Elongation factor Tu (EF-Tu).
(TUFA OR STWA345) OR STY4353) AND (TUFB OR STM4146 OR STY3739).
Salmonella typhimurium, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%; Score 111; DB 1; Length 393; 90.5%; Pred. No. 8.6e-11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam: PF00009, GTP_FEFTU; 1. Pfam: PF03144; GTP_EFTU_D2; 1. Pfam: PF03143; GTP_EFTU_D3; 1. PRIWTS; PR0315; ELONGATHECT. PROSITE; PS00301; EFACTOR_GTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFERTKPHVNVGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32739; AAC22236.1; -. EMBL; U32746; AAC22292.1; -. HSSP; P02990; 1ETU.
Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
25
84
138
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
80
81
81
```

ASSOCIATED WITH AMINOACYL-TRNA BINDING

81

```
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                              EFTA_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
     FT
                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P02990; IEFC.
Stydene; SG10403; tufA.
Stydene; SG10404; tufA.
Stydene; SG10404; tufA.
Stydene; SG10401; tufA.
InterPro: IPR004160; GTP_EFTU.
InterPro: IPR004160; GTP_EFTU.D2.
InterPro: IPR004160; GTP_EFTU.D3.
Ffam; PP00109; GTP_EFTU.D3.
Pfam; PP03144; GTP_EFTU.D3: 1.
Pfam; PF03143; GTP_EFTU.D3: 1.
PRNINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein blosynthesis; GTP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-S. Typhi; STRAIN=CT18; MEDLINE-21534947; PubMed=11677608; MEDLINE-21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L. Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cretwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica servoar Typhi CT18";
                                                                                                                SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609; MCCLelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                        "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLIALIDAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FF-1A SUBFAMILY.
"The role of EF-Tu and other translation components in determining translocation step size.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -I- FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

METHYLATION (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omplete proteome.

BY SIMILARITY.
                                             Biochim. Biophys. Acta 1050:274-278(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE008858; AAL22308.1; EMBL; AE008893; AAL22974.1; EMBL; AL627279; CAD09494.1; EMBL; AL627281; CAD08168.1; PIR; S13560; S13561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X55116; CAA38912.1; -. EMBL; X55117; CAA38913.1; -.
                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
84
138
56
382
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INIT_MET
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
  TILITE AND BEAR AND B
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. S21. U.S.A. 98:3460.3465(2001).
-!- FUNCTION: THIS PROPEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBBUIT: MONOMER (BY SIMILARITY).
-:- SUBBUIT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: CYtoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                ASSOCIATED WITH GUANOSINE NUCLEOTIDE
BINDING ACTIVITIES (BY SIMILARITY).
2833061693363BC4 CRC64;
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.2%; Score 111; DB 1; Length 394; 90.5%; Pred, No. 8.6e-11;
                                                                                                                                                 90.2%; Score 111; DB 1; Length 393; 90.5%; Pred. No. 8.6e-11; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TP (BY SIMILARITY).

TP (BY SIMILARITY).

0C704405CF5E9A4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-A (EF-Tu-A).
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                          394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE006173; AAK03441.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IRR004160; GTP_EFTU_D2.
Pfam; PF00109; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21145866; PubMed-11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP
                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43353 MW;
                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                    2 KEKFERTKPHVNVGTIGHVDH 22
                                                                             43152
                                                                                                                                                      Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella multocida
                                                                        393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS.
                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUFA OR PM1357
                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTA_PASMU
P57939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PM70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                          BINDING
```

QF.

```
Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.; "The chloroplast genome of a chlorophyll a+c-containing alga,
                                                                   Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBL_TaxID=2839;
                                                                                                                                                               Odontella sinensis.";
Plant Mol. Biol. Rep. 13:336-342(1995).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
    15-DEC-1998 (Rel. 37, Last annotation update) Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                    BIOSYNTHESIS.
                                                           Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_NEPOL Q9TKZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNIB_AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
EFTU_NEPOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCOCCOS OCCOCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                          May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.2%; Score 111; DB 1; Length 394; 90.5%; Pred. No. 8.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
CS85C9DFA6935559 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00109; GTP_EFU; I.
Pfam; PF03144; GTP_EFU; I.
Pfam; PF03143; GTP_EFTU_D2; I.
PRINTS; PR00315; ELONGATNET.
PROSITE; PS00301; EFACTOR_GTP; I.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUFB OR PM1746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 33, Created)
(Rel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                MEDLINE-21145866; PubMed-11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE006212; AAK03830.1; -.
InterPro; IPR000795; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
43375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KEKFERTKPHVNGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                         Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHESIS
                                                                                                                                                                                                                               NCBI_TaxID=747;
                                                                                            EFTB_PASMU
P57966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTU_ODOSI
P49462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP_BIND
NP_BIND
SEQUENCE
                                                                                 EFTB_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFTU_ODOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                            g
  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
-1- SUBCELLULAR LOCATION: Chloroplast.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.6%; Score 109; DB 1; Length 409; 90.5%; Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 3DDBBBAC190C2009 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nephroselmis olivacea.
Chloroplast.
Eukaryota: Viridiplantae; Chlorophyta; Prasinophyceae;
Chlorodendrales; Chlorodendraceae; Nephroselmis.
NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Blongation factor Tu (EFF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                          Mendel; 13232; ODOSI;TufA;1...
InterPro; IPRO004795; GTP_EFTU_D2.
InterPro; IPRO04161; GTP_EFTU_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 REKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                               EMBL; Z67753; CAA91621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
```

ŏ a 12 K E

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
EF-TU/EF-1A SUBFAMILY.
                               -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 0FAF86F46938AAA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nastr Folgo LEFO.
InterPro; PRO04161; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU.D2.
InterPro; IPR004161; GTP_EFTU.D2.
InterPro; IPR004160; GTP_EFTU.D3.
Pfam; PF03144; GTP_EFTU.D2; 1.
Pfam; PF03144; GTP_EFTU.D2; 1.
Pfam; PF03143; GTP_EFTU.D3; 1.
PROSTTE; PR00315; ELONGANRET.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.8%; Score 108; DB 1;
90.5%; Pred. No. 2.7e-10;
tive 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF Dongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                       SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96425873; PubMed=8828215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y17167; CAA76676.1; -. EMBL; AL139075; CAB75108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 AA; 43593 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KEKFSRNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
85
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. NP_BIND 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02990; 1EFU
                                                                                                            BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTU_NEIGO
P48864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_NEIGO
SO DE RESERVANTE DE RESERVANTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HD DDT ACCOUNT COLOR COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Turber are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                 Turmel M., Otis C., Lemieux C.; "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERMINENCE 1168;
MEDLINE-2015.0912; Pubmed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.W., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                        -:- SUBCELLULAR LOCATION: Chloroplast.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thies F., Giegerich G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
A7A9B0A6E99C1B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU. 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
GTP-binding factor; Protein biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUPF OR TUFB OR CJ0470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reveals hypervariable sequences.";
                               MEDLINE=99398694; PubMed=10468594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF137379; AAD54821.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 REKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P02990; 1ETU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTU_CAMJE
069303;
                                                                                                                                                                                      genomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFTU_CAMJE
```

g

ò

ó;

Gaps

œ

```
InterPro; IPR000795;
                   InterPro;
                                                                                                                                                                        NP_BIND
SEQUENCE
                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes."
   ò
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Mitochondrial.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97311393; PubMed-9168110;
Lang B.F., Burger G., O'Kelly C.J., Cedergren R., Golding G.B.,
Lemieux C., Sankoff D., Turmel M., Gray M.W.;
"An ancestral mitochondrial DNA resembling a eubacterial genome
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                     Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                        GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
F96799BE63520444 CRC64;
                                                                                                                                                                                                                                                                                           Elongation factor; Protein biosynthesis; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                     87.0%; Score 107; DB 1; Le
85.7%; Pred. No. 3.9e-10;
"Hematches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu, mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; core jakobids; Reclinomonas.
NCBL_TaxID=48483;
                                                                                                                                                       InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                        43084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF007261; AAD11872.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KEKFERSKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                              EMBL; L36380; AAB41517.2; -.
HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    miniature.";
Nature 387:493-497(1997).
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 87.0
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reclinomonas americana.
                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                                                                                                                                          394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=ATCC 50394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_RECAM
021245;
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                          NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFTU_RECAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SGA1;
MEDLINE=94586062; PubMed=8085791;
Ludwig W., Neumaiar J., Klugbauer N., Brockmann E., Roller C.,
Klugbauer S., Reetz K., Schachtner I., Ludwigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
Phylogenetic relationships of Bacteria based on comparative sequence
analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                  Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding. NP_BIND 19 26 GTP (BY SIMILARITY). NP_BIND 18 6 GTP (BY SIMILARITY). SEQUENCE 394 AA; 43627 MW; 428202ADF3DBC4EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- SUBCELLIULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΘF
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Cystobacteraceae; Stigmatella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bremaud L., Fremaux C., Laalami S., Cenatiempo Y.; "Genetic and molecular analysis of the tRNA-tufB operon of the myxobacterium Stigmatella aurantiaca."; Nucleic Acids Res. 23:1737-1743(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antonie Van Leeuwenhoek 64:285-305(1993).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                          Score 107; DB 1;
Pred. No. 3.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 AA
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95303606; PubMed=7784178;
                                                  Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
IPR000795; GTP_EFTU.
IPR004161; GTP_EFTU_D2.
IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTU_STIAU STANDARD; F P42479; 053775; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1997 (Rel. 35, Last sequin-16-OCT-2001 (Rel. 40, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                          87.0%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X82820; CAA58029.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 18-396 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            3 KEKFERTKPHCNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stigmatella aurantiaca
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUF OR TUFB.
```

```
STRAIN=MADRID E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
85
139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTU_RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P48865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Lihher K.D., Garrert M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Fvidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bachleitner M., Ludwig W., Stetter K.O., Schleifer K.H.; "Nucleotide sequence of the gene coding for the elongation factor Tu from the extremely thermophilic eubacterium Thermotoga maritima."; FEMS Microbiol. Lett. 48.115-120(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tiboni O., Cantoni R., Creti R., Cammarano P., Sanangelantoni A.M.; "Phylogenetic depth of Thermotoga maritima inferred from analysis of the flus gene: amino acid sequence of elongation factor G and organization of the Thermotoga str operon."; J. Mol. Evol. 33:142-151(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 107; DB 1; Length 396;
Pred. No. 4e-10;
); Mismatches 2; Indels
                                                                                                                                                                                                          GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
R -> P (IN REF. 2).
E -> D (IN REF. 2).
P -> R (IN REF. 2).
P -> R (IN REF. 2).
V -> L (IN REF. 2).
W -> L (IN REF. 2).
W -> L (IN REF. 2).
                                                                                                                                                                                             Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome sequence of Thermotoga maritima."; Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
NCBL_TaxID=2336;
                              InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PR03175; PR00315; ELONGATNFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-13 FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-92015266; PubMed=1920450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-MSB8 / DSM 3109;
MEDLINE-89232666; PubMed-2714630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P13537;
0J-JAN-1990 (Rel. 13, Created)
30-MAX-2000 (Rel. 39, Last sequing Control (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 KEKFERNKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                         43367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%;
90.5%;
EMBL; X76870; CAA54197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                         372
376
390
396 7
                HSSP; P02990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUF OR TM1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFTU_THEMA P13537;
                                                                                                                                                                                                            NP_BIND
NP_BIND
NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_THEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οg
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOORDER TO THE SET OF THE SET O
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-MADRID E;
MEDLINE-97047977; PubMed-8892818;
SYVANEN A., AnLr! H., Jamal A., Andersson S.G.E., Kurland C.G.;
"A chimeric disposition of the elongation factor genes in Rickettsia
                                                                                                        SUBCERLULAR LOCATION: CYTOPLESSIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                        AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.0%; Score 107; DB 1; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> V (IN REF. 1).
73F479FE4F69E9A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro: IRR000795; GTP_EFTU.
InterPro: IRR004161; GTP_EFTU.D2.
InterPro: IRR004160; GTP_EFTU_D2.
Pfam: PF03144; GTP_EFTU_D3.
Pfam: PF03144; GTP_EFTU_D2; 1.
Pfam: PF03143; GTP_EFTU_D2; 1.
Pfam: PF03143; GTP_EFTU_D3; 1.
PROSTIES; PR00315; ELONGATNECT.
Elongation factor: Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
G -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF OR RP661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4e-10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 AA
                                                                                      SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 178:6192-6199(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KEKFVRTKPHVNVGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44467 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M27479; AAA27415.1; -.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                           -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/DE-1A SUBFAMILY.
                                                                                                                                ΟF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krasny L., Mesters J.R., Tieleman L.N., Kraal B., Fucik V., Hilgenfeld R., Jonak J.;
Hilgenfeld R., Jonak J.;
"Structure and expression of elongation factor Tu from Bacillus stearothermophilus.";
J. Mol. Biol. 283:371-381(1998).
                     Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H., "The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                    Mature 407:757-762(2000).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-MINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%; Score 106; DB 1; Length 394; 90.5%; Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, 234275; CA844029.1; --
EMBL, AE001151; AAF30935.1; --
EMBL, AE001151; AAF30935.1; --
HSSP, P02990, IETU.
InterPro; IPR004161; GTP_EFTU.D2.
InterPro; IPR004161; GTP_EFTU.D2.
InterPro; IPR004160; GTP_EFTU.D2.
Pfam; PF03144; GTP_EFTU.D3.
Pfam; PF03144; GTP_EFTU.D3: 1.
Pfam; PR03143; GTP_EFTU.D3; 1.
PROSITE; PR00315; ELONGATHECT.
PROSITE; PS00310; ERACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 80A887B6C59883E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Geobacillus.NCBL_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CCM 2184;
MEDLINE-98443240; PubMed-9769211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
136
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
                                                                                                                                                                          BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTU_BACST
050306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 17
EFTU_BACST
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                       -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLIAGA LOCATION: CYTOPLASMIC.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                O.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thesis (1994), Heinrich-Heine University / Duesseldorf, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                      Nature 396:133-140(1998).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBL_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 1; Length 35-Pred. No. 5.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
S -> T (IN REF. 1).
RAT -> ELQ (IN REF. 1).
W; 510FB2997E389BBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; PR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF003144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINFCT.
Elongation factor; Protein blosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
TUF OR UU522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 33697 / SEROVAR 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z54170; CAA90881.1; -. EMBL; AJ235272; CAA15101.1; HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN*SEROVAR 3;
                                                                                                                                                                        BIOSYNTHESIS.
                                                                                     mitochondria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_UREPA
P50068;
```

CONFLICT

NP_BIND NP_BIND NP_BIND

SEQUENCE

RESULT 16 EFTU_UREPA

à g Bruex A.;

ö

Gaps

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93188701; PubMed-8446028; Menorar Bergh S., Chanteau S., Doucet-Populaire F., Honora N.T., Bargh S., Chanteau S., Doucet-Populaire F., Eiglmeier K., Garnier T., Georges C., Launois P., Limpaiboon T., Newton S., Niang K., del Portillo P., Ramesh G.R., Reddi P., Ridel P.R., Sittisombut N., Wu-Hunter S., Cole S.T., "Nucleotide sequence of the first cosmid from the Mycobacterium legrae genome project: structure and function of the Rif-Str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94375410; PubMed=8089081;
Dhandayuthapani S., Banu J.M., Kashiwabara Y.;
"Cloning and sequence determination of the gene coding for the elongation factor Tu of Mycobacterium leprae.";
J. Biochem. 115:664-669(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silbak F., Bercovier H.; "Nucleotide sequence of Mycobacterium leprae elongation factor
                                                                                                                                                                                 Cursend an emc.

REMEL, X77034; CAA44323.1; -.

REMEL, X77034; CAA44323.1; -.

RESP; PO2990; LETU.

DR InterPro; IPR000155; GTP_EFTU.

DR Ffam; PP00009; GTP_EFTU. D2.

DR Ffam; PP00144; GTP_EFTU. D2.

DR PERT, PR00145; GTP_EFTU. D3.

DR PRINTS; PR00315; EFTU.D2; 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

DR PROSITE; PS00301; EFACTOR_GTP; 1.

RW BLONG ACCOUNTY BROUGHT BROWN BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.2%; Score 106; DB 1; L 90.5%; Pred. No. 5.8e-10; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 21:3327-3327(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93341950; PubMed=8341612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 7:207-214(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elongation factor Tu (EF-Tu) TUF OR ML1877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KAKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EF-Tu) gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTU_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P30768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 19
EFTU_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ρp
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                 SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SÜBÜNIT: MONOMER (BY SIMILARITY).
-1- SÜBÜLLÜLAR LÖCATION: CYLOPLASMIC.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/ZE-1A SÜBFÄMLIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C., Klugbauer S., Reetz K., Schachtner I., Ludwigsen A., Bachleitner M., Fischer U., Schleifer K.H.;
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative sequanalysis of elongation factor Tu and ATP-synthase beta-subunit Antonie Van Leeuwenhoek 64:285-305(1993).

I- FUNCTION: THIS PROFEN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROFEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 1; Length 395;
Pred. No. 5.8e-10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTP (BY SIMILARITY).
71B08165E7FB42C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elongation factor; Protein biosynthesis; GTP-binding. NP_BIND 19 26 GTP (BY SIMILARITY). NP_BIND 81 85 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR000795; GTP_EFTU.
InterPro: IPR004161; GTP_EFTU_D2.
InterPro: IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; I.
Pfam; PF03144; GTP_EFTU_D2; I.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 13059 / AS019;
MEDLINE-94368062; PubMed-8085791;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ000260; CAA03976.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq)
16-OCT-2001 (Rel. 40, Last anno
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 AA; 43290 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_CORGL P42439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_CORGL
                                                                                                              <del>!</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

ö

Gaps

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> VYLTSWSHLTSPT
                                                        COIE S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Mutphy L., Oliver K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.,

"Massive gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001).

- FUNCTION: THIS PROPEIN PROMOTES THE GTP-DEPENDENT BINDING OF

AMINOACKI-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EE-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106; DB 1; Length 39
Pred. No. 5.8e-10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GVPYILVALNKSDAVDDEELLELV ->
PWTRNYSSLS (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> P (IN REF. 3).
D9CB88343C642778 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> V (IN REF. 2)
G -> A (IN REF. 2)
R -> P (IN REF. 3)
                                            MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00009; GTP_EFTU; 1. Pfam; PF001144; GTP_EFTU D2; 1. Pfam; PF03143; GTP_EFTU D3; 1. PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L13276; AAA71969.1; -.
EMBL; Z14314; CAA78674.1; -.
EMBL; D13869; BAA02982.2; -.
EMBL; AL583923; CAC30831.1; -.
PIR; S34954; S34954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Μ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KAKFERTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.2
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
87
141
152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                À,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
NP_BIND 19
              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
396 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leproma; ML1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ETU MYCTU STANDARD; PRT; 396 AA P31501; Q50823; P95031; 01-JUL-1993 (Rel. 26, Created) 01-JUL-1993 (Rel. 26, Last sequence update)

EFTU_MYCTU

HARE.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                       Carlin N.I.A., Loefdahl S., Magnusson M.;
"Monoclonal antibodies specific for elongation factor Tu and complete
nucleotide sequence of the tuf gene in Mycobacterium tuberculosis.";
Infect. Immun. 60:3136-3142(1992).
                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOSYNTHESIS.
SUBUNTT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONG TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                           MEDITNE-98295987; pubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglander K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Coliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROFEIN PROMOTES THE GTP-DEPENDENT BINDING
-MINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
THO OR RV0685 OR MT0713 OR MTCX210.02.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X63539; CAA45102.1; -.
EMBL; X63539; CAA45101.1; ALT_INIT.
EMBL; 284395; CABO6471.1; -.
EMBL; AE006965; AAK44939.1; -.
                                                                                                                                                                                                  MEDLINE=92347983; PubMed=1639483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRAM: PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; MT0713; -...
TUBETCULIST; RV0685; -...EFTU.
INTERPRO; IPR000795; GTP_EFTU.
INTERPRO; IPR004161; GTP_EFTU_D2.
INTERPRO; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A44795; A44795.
HSSP; P02990; 1ETU.
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                   STRAIN=ERDMANN;
                                                                                                                                                                                                                                                                                                                                              STRAIN-H37RV;
```

```
PROSITE; PS00301;
                                                                                                                                                                                                                 RESULT 22
EFTU_PSEAE
                                                                                                                                                                                                                                               KKK
KK
FT
FT
SO
                                                                                                                                                              ŏ
                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                         ó
                                                                                                                                                                                                                                                                                     Bacteria; Protechacteria; beta subdivision; Comamonadaceae; Thiomonas.
NCBL_raxID=36860;
                                                                                                                                                                                                                                                                                                                                            MEDLINE=94368062; pubMed=8085791;
Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C.,
Klugbauer S., Reetz K., Schachtner I., Ludvigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative sequence
analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLIOLAR LOCATION: CYtoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                    Length 396;
                                                                                                         2; Indels
                    26 GTP (BY SIMILARITY).
87 GTP (BY SIMILARITY).
141 GTP (BY SIMILARITY).
43593 MW; 85F9012F364692FF CRC64;
 Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                   86.2%; Score 106; DB 1;
ilarity 90.5%; Pred. No. 5.8e-10;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                     EFTU_THICU STANDARD; PRT; 396 AA. P42481; 050556; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 10-CCT-2001 (Rel. 40, Last annotation update) Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                        Antonie Van Leeuwenhoek 64:285-305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P02990; 1ETU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINECT.
                                                                                                                               22
                                                                                                                                         EMBL; X76871; CAA54198.1; -. EMBL; U78300; AAB87734.1; -.
                                                                                                                               2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                 Thiobacillus cuprinus.
                      19
83
138
396 AA;
                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM 5495;
                     NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                 RESULT 21
EFTU_THICU
                                                                                                                                                                                                         ð
                                                                                                                                                  용
  SELLES
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Fittute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLIND=2043737; Pubmdcd-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBGNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYCOPLASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-12 FROM N.A.
MEDLINE=88303352; Pubbled=3136442;
Hughes M.A., Jones D.S.;
Hughes M.A., Jones D.S.;
A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four of which are linked to an EF-Tu gene.";
Nucleic Acids Res. 16:7193-7193(1988).
-1. FUNCTION: THIS PROTEIN PROMOTES THE GIP-DEPENDENT BINDING OF AMINOACYL_TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                           Length 396;
L; EFACTOR_GTP; 1.

26 GTP (BX SIMILARITY).

85 GTP (BX SIMILARITY).

139 GTP (BY SIMILARITY).

139 GTP (BY SIMILARITY).

109 A -> G (IN REF. 2).

383 G -> A (IN REF. 2).

383 G -> AG (IN REF. 2).

384 GA -> AG (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                     86.2%; Score 106; DB 1;
85.7%; Pred. No. 5.8e-10;
ive 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE004843; AAG07665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X07950, CAA30775.1; -.
PIR, S01222, S01222.
InterPro, IPR000795, GTP_EFTU.
                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KSKFERTKPHVNVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                     Query Match 86.2
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                Elongation factor, PNP_BIND 19
NP_BIND 81
NP_BIND 136 1
                                                              19
81
136
109
383
387
396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TUFB OR PA4277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTU_PSEAE
P09591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas.
                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
SEQUENCE
```

ö

Gaps

ó

```
Ludwig W., Weizenegger M., Betzl D., Leidel E., Lenz T., Ludvigsen A., Moellenhoff D., Wenzig P., Schleifer K.H.;
"Complete nucleotide sequences of seven eubacterial genes coding for the elongation factor Tu: functional, structural and phylogenetic evaluations.";
Arch. Microbiol. 153:241-247(1990).

A.F. BUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL.TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNT: MONOMER.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
PIR; F60663; F60663.
                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                              Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.2%; Score 106; DB 1; Length 398; 85.7%; Pred. No. 5.8e-10; tive 3; Mismatches 0; Indels
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 82399826C6C08E90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elongation factor; Protein biosynthesis; GTP-binding
                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA.
                                                                                                                                                                                    398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P02990, IEPU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGARNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90240875; PubMed=2110445;
                                                                                     22
                                                                                                    3 KAKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44013 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 KEKYDRSKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                    2 KEKFNRTKPHVNIGTIGHVDH
                                                          Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                    Streptococcus oralis.
                             Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1303;
                                                                                                                                                                                                                                                                                                              Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                  EFTU_STROR P33170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFTU_STRPY
P82559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
EFTU_STRPY
                                                                                                                                                        24
                                                                                                                                                                       EFTU_STROR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAPE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBDATT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces cinnamoneus.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_FaxID=53446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cappellano C., Monti F., Sosio M., Donadio S., Sarubbi E.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROPEIN PROMOTES THE GIP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                             Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                        19 26 GTP (BY SIMILARITY).
81 85 GTP (BY SIMILARITY).
136 139 GTP (BY SIMILARITY).
397 AA: 43369 MW; A019D5BF8EBBAB942 CRC64;
        InterPro; PR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRNUTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein blosynthesis; GTP-binding;
                                                                                                                                                                                                           Score 106; DB 1; I
Pred. No. 5.8e-10;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (ER-Tu).
                                                                                                                                                                                                                                                                                                                                                                   397 AA.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
 InterPro; IPR004161; GTP_EFTU_D2
                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                3 KEKFERNKPHVNVGTIGHVDH 23
                                                                                                                                                                                                           86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X98831; CAA67349.1; -
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                           Complete proteome.
                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-TUE89;
                                                                                                                                                                                                                                                                                                                                                                 EFTU_STRCJ
P95724;
                                                                                                                                     NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                       RESULT 23
                                                                                                                                                                                                                                                                                                                                                     EFTU_STRCJ
Q
                                                                                                                                                                                                                                                                 ð
```

ö

Gaps

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                      STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Maneko T., Nakamura Y., Sato S., Kawashima K., Kimura T.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochiuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                        Mesorhizobium loti.";

DNA Res. 7:331-338(2000)

-!- FUNCTION: THIS PROPEND PROMOTES THE GTP-DEPENDENT BINDING OF

AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
Elongation factor Tu (EF-Tu).
(TUDA OR MLR0263) AND (TUFB OR MLR0288).
Rhizoblum loti (Mesorhizoblum loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma gallisepticum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 036718E6A48B48A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00301; EFACTOR_GTP; 1.
on factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 105; DB 1; Le
90.5%; Pred. No. 8.4e-10;
uiematches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO00795; GTP_EFTU.
InterPro; IPRO04161; GTP_EFTU_D2.
InterPro; IPRO04161; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D1.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP002994; BAB47886.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KGKFERTKPHVNIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP002994; BAB47904.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 AA; 42713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
80
134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSYNTHESIS
                                                                                                              NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFTU_MYCGA
P18906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
EFTU_MYCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                      STRAIN=SF370 / ATCC 700294 / Serotype M1;
MEDLINE=21192664; PubMed=11296296;
Ferretti J.J., McShan W.M., Addic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JRS4 / Serotype M6;
Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
VanBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBGUNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLUAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-2000) to the SWISS-PROT data bank.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006516; AAK33586.1; -.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU.D.
Pfam; PF00109; GTP_EFTU.D.
Pfam; PF03144; GTP_EFTU.D.
Pfam; PF03143; GTP_EFTU.D.; 1.
Pfam; PF03145; GTP_EFTU.D.; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP (BY SIMILARITY).

FP (BY SIMILARITY).

FP (BY SIMILARITY).

21E0B20A8DD21AFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.2%; Score 106; DB 1;
85.7%; Pred. No. 5.8e-10;
ive 3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 AA
                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP
GTP
GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA; 43855 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KEKYDRSKPHVNIGTIGHVDH 23
           factor Tu (EF-Tu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                   Streptococcus pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
NP_BIND 19
                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                            NCBI_TaxID=1314;
        Elongation fac
FUF OR SPY0611
                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_RHILO
Q981F7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
NP_BIND
```

ö

Gaps

ö

RESULT 26 EFTU_RHILO

a 검점점당

ò g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                  -i- SUBUNIT: MONOMER.
-i- SUBCELLIAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                           Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=42684;
                                                                                               OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mikulik K., Zhulanova E., "Sequencing of the tufl gene and the phosphorylation pattern of "Sequencing of the tufl gene and differentiation in Streptomyces EF-Tul during development and differentiation in Streptomyces collinus producing kirromycin.";
Biochem. Biophys. Res. Commun. 213:454-461(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                        SUDMITTED (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 105; DB 1; Length 397;
85.7%; Pred. No. 8.5e-10;
iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GTP (BY SIMILARITY).
B7 GTP (BY SIMILARITY).
141 GTP (BY SIMILARITY).
43781 MM; D27DF957DF775 CRC64;
                                      Saunders D.C., Harris D., Cerdeno A.M., Parkhill J.,
Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-1 (EF-Tu-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 AA
                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X77039; CAA54329.1; --
EMBL, AL161691; CAB81853.1; --
PIR; 841335; 841335.
HSSP: P003990; LETU.
INTERPRO; IPRO00795; GTP_EFTU.
INTERPRO; IPRO04160; GTP_EFTU_D2.
InterPRO; IPRO04160; GTP_EFTU_D2.
Pfan; PF00109; GTP_EFTU_D2.
Pfan; PF03144; GTP_EFTU_D2; 1.
Pfan; PF03144; GTP_EFTU_D2; 1.
PRNNTS; PR00315; ELONGATNFCT.
PROSITE; PS00301; EPACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BSM 40733;
MEDLINE=95374503; Pubmed=7646499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces collinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 1
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family.
                                                                                                                                 BIOSYNTHESIS
                        STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (
01-NOV-1997 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFT1_STRCU Q53871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONIB_NN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 29
EFT1_STRCU
     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                 MEDLINE-90098800; PubMed-2602129; Inamine J.M., Loechel S., Hu P.C.; Inamine J.M., Loechel S., Hu P.C.; Mucleic decide sequence of the tuf gene from Mycoplasma gallisepticum."; Nucleic Acids Res. 17.10126-10126(1989).

- PUNCTION: THIS PROFIEN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROFIEN
                                                                                                                                                                               -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLIULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2) / M145;
MEDLINE=95002174; PubMed=7918656;
van Wezel G.P., Woudt L.P., Vervenne R., Verdurmen M.L.,
Vijgenboom E., Bosch L.;
"Cloning and sequencing of the tuf genes of Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.4%; Score 105; DB 1; Length 394; llarity 81.0%; Pred. No. 8.4e-10; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
963E8B93216279F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00009; GPP_EFTU. 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR0315; ELONGATNFCT.
PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-DGTgation factor Tu-1 (EF-Tu-1).
TUF1 OR SCD40A.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1219:543-547(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P02990; IEEU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 KERFDRSKPHVNIGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16462; CAA34482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S14910; EFYMTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                    BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFT1_STRCO
P40174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
```

ò g ö

Gaps

us-09-488-737-1.rsp

```
-! - SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                           43918 MW;
                                                                                                                                                                                                                                                                                                                                                                             2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                           3 KAKFERTKPHVNIGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.73
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces ramocissimus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                       26
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ramocissimus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFT2_STRRA
                                                                                                                                                                                                                                                                 NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P29543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFT2_STRRA
 å
                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                    SUBGUNIT: MONOMER.
SUBCELLULAR LOCATION: CYLOPLASMIC.
PTM: PHOSPHORYLATED ON THREONINE AND SERINE.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: CYtoplasmic.
-:- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/DE-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiology 140:983-998(1994).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDIINE-94282341; Pubmed-8012612;
Vijgenboom E., Woudt L.P., Heinstra P.W.H., Rietveld K.,
Van Haarlem J., van Wezel G.P., Shochat S., Bosch L.;
"Three tuf-like genes in the Kirromycin producer Streptomyces
                                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

PHOSPHORYLATION (BY SIMILARITY).

D72A4054CA2EB567 CRC64;
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%; Score 105; DB 1; Length 397; 85.7%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                             InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF000099; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS, PR00315; ELONGATNFCT.
PROSTTE; PS00310; EFACTOR_GTP; 1.
Blongation factor; Protein blosynthesis; GTP-binding; whitigene family; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-1 (EF-Tu-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         43879 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KAKFERTKPHVNIGTIGHIDH 23
                                                                                                                                                                                        EMBL; S79408; AAC60496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces ramocissimus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                               138
386
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFT1_STRRA P29542;
                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFT1_STRRA
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiology 140:983-998(1994).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94282341; PubMed-8012612; Vijgenboom E., Woudt L.P., Heinstra P.W.H., Rietveld K., van Haarlem J., van Wezel G.P., Shochat S., Bosch L.; "Three tuf-like genes in the kirromycin producer Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 397;
                                                                                                                                                                                                                                                                                                                        EMBL; X67057; CAA47442.1; -..
PIR; S23908; S23908.
HSSP; P02990; B120.
InterPro; IPR00795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D2.
Pfam; PF03144; GTP_EFTU; 1..
Pfam; PF03144; GTP_EFTU_D2; 1..
Pfam; PF03145; GTP_EFTU_D3; 1..
PRINTS; PR00315; ELONGATNFCT.
PROSITE; PS00315; ELONGATNFCT.
PROSITE; PS00301; ERACTOR_GTP; 1..
PROSITE; PS00301; ERACTOR_GTP; 1..
PROSITE; PS00301; ERACTOR_GTP; 1..
PROSITE; PS00301; ERACTOR_GTP; 1..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 5442152843D4E306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 105; DB 1;
85.7%; Pred. No. 8.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu-2 (EF-Tu-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
```

us-09-488-737-1.rsp

factor;

```
Elongation f
                                NP_BIND
    KY
FT
SO
SO
                                                                                                                                                                                                qq
                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLIAUGA LOCATION: CYLOPLASMIC.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 10762 / CCM 3239;
Weiser J., Kormanec J., Potuckova L., Homerova D., Vohradsky J.,
Novotna J., Kalachova L.;
Submitted (JUW-1997) to the EMBL/GenBank/DDBJ databases:
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                  85.4%; Score 105; DB 1; Length 397;
85.7%; Pred. No. 8.5e-10;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                          P (BY SIMILARITY).
P (BY SIMILARITY).
B77172DD423623AD CRC64;
                                                                                                                                                                Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 AA.
                        HSSP; PO2990; IETU.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03144; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF03009; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
PR03175; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                          GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF007125; AAB62702.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                        44268 MW;
                                                                                                                                                                                                                                                                                                                                            2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created 15-JUL-1998 (Rel. 36, Last set 16-QUL-2001 (Rel. 40, Last an Elongation factor Tu (EF-Tu).
EMBL; X67058; CAA47443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces aureofaciens.
                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                 ; $23909.
                                                                                                                                                                                                         83
138 1
397 AA;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                             Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998
15-JUL-1998
16-OCT-2001
              PIR; S23909
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFTU_STRAU
033594;
                                                                                                                                                                                                                        NP_BIND
SEQUENCE
                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                   EFTU_STRAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                              õ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Montandon P.-E., Stutz E.; "Notation gracilis chloroplast genome region "Nucleotide sequence of a Euglena gracilis chloroplast genome region coding for the elongation factor Tu; evidence for a spliced mRNA."; Nucleic Acids Res. 11:5877-5892(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Chloroplast.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88040410; PubMed-3118328;
Montandon P.-E., Knuchel-Aegerter C., Stutz E.;
"Euglena gracilis chloroplast DNA: the untranslated leader of tufa-
ORF206 gene contains an intron.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genes for the ribosomal proteins S12 and S7 are clustered with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the gene for the EF-Tu protein on the chloroplast genome of Euglena gracilis.",
                                                                                                                                            ö
                                                                                                           Score 105; DB 1; Length 397;
Pred. No. 8.5e-10;
1; Mismatches 2; Indels
Protein biosynthesis; GTP-binding.
26 GTP (BY SIMILARITY).
87 GTP (BY SIMILARITY).
1411 GTP (BY SIMILARITY).
43509 MW; A22F12F0E3008EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                   409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORF206 gene contains an intron.";
Nucleic Acids Res. 15:7809-7822(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 12:2851-2859(1984).
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
SEQUENCE OF 1-28 FROM N.A.
MEDLINE-84169577; PubMed-6324129;
Montandon P., Stutz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-83299257; PubMed-6310519;
                                                                                                                                                                        2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                          3 KAKFERTKPHVNIGTIGHIDH 23
                                                                                                             85.4%;
                                               141
43509 N
                                                                                                           Query Match 85.4
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                   STANDARD;
                 19
83
138 1
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Euglena gracilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION
                                                                                                                                                                                                                                                                 EFTU_EUGGR
ID EFTU_EUGGR
                                             NP_BIND
SEQUENCE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Freischmann R.D., Bult G.J., Kerlavage A.R., Sutton G., Kelley J.M., Frietchmann J.L., Weidman J.F., Samoll K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inamine J.M., Loechel S., Hu P.-C.; "Nucleotide sequence of the tuf gene from Mycoplasma genitalium."; Nucleic Acids Res. 17:10127-10127(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOJANENCE OF 196-309 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmde-8253680;
PEterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                               GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

I -> M (IN REF. 2).

O9B73EADCAODF5F6 CRC64;
                                                                                                                                                                                                                               Interpro; IPR000795; GTP_EFTU.
Pfam; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGAINFCT.
PROSTITE; PS00301; EFACTOR GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 1; L
Pred. No. 1.2e-09;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTU_MYCGE STANDARD; PRT; 394 AA. P13927; 049360; 10.1JAN-1990 (Rel. 13, Created) 01.JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) TUF OR MG451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2: Mismatches
                                                                                                                                                                      EMBL; AP001119; BAB13219.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE-90098801; Pubmed-2602130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 175:7918-7930(1993)
                                                                                                                                                                                                                                                                                                                                                               19 26 GT
81 85 GT
136 139 GT
89 89 I
394 AA; 43465 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KEKFQRLKPHINVGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2097;
                                                                                                                                                                                        EMBL; Y12307; CAA72974.1; -. HSSP; P02990; 1ETU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                             Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                          ONIA_9N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 35
EFTU_MYCGE
      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GIP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FE-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98242088; PubMed=9580987;
MEDLINE=98242088; PubMed=9580987;
Brynnel E.U., Kurland C.G., Moran N.A., Andersson S.G.;
"Evolutionary rates for tuf genes in endosymbionts of aphids.";
Mol. Biol. Evol. 15:574-582(1998).
-!- FUNCTION: THIS PROTEIN PROWOTES THE GTP-DEPENDENT BINDING OF
ANINOMACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

METHYLATION (MOND-) (PROBABLE).

C803740422FFEB84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 105; DB 1; Length 409;
81.0%; Pred. No. 8.8e-10;
tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                            Elongation factor; Protein biosynthesis; Chloroplast; GTP-binding; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
  or send an email to license@isb-sib.ch)
                                EMBL; 211874; CAA77904 11; EMBL; X00044; CAA2925.1; EMBL; X00044; CAA2925.1; EMBL; X00810; CAA50087.1; EMBL; X00810; CAA50087.1; EMBL; X00480; CAA5159.1; FRFCT. FIR: S02254; S02254; S02254; S02254; S02254; S02254; FRFCT. FRSP; PO2990; 1ETU. InterPro; IPR000795; GTP_EFTU. InterPro; IPR004161; GTP_EFTU. InterPro; IPR004160; GTP_EFTU. InterPro; IPR004160; GTP_EFTU. Fram; PF03144; GTP_EFTU_D2; Pfam; PF03144; GTP_EFTU_D2; Pfam; PF03144; GTP_EFTU_D2; Pfam; PF03144; GTP_EFTU_D3; Pfam; PF03143; GLONGATNFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 26 GTI
81 85 GTI
136 139 GTI
57 57 MEI
409 AA; 45062 MW; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ROKFERTKPHINIGTIGHVDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUF OR BU526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTU_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFTU_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
```

g ò

DATE OF THE SET OF THE

```
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                           BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
81
136
12
12
122
136
198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=292;
                                                               pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_BURCE
P33167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTU_BURCE
1D EFTU_B
1D 973167
DT 01-0CT
DT 16-0CT
DE ELONG
DR TUF.
0C BURKhC
0C BURKhC
0C BURKhC
0C BURKhC
0C ROCC
NC ROCC
NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                         SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELIULAR LOCATION: CYCOPLASMAC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/FE-1A SUBFAMILY.
FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yogev D., Sela S., Bercovier H., Razin S.;
"Nucleotide sequence and codon usage of the elongation factor
TYUEF-TU) gene from Mycoplasma pneumoniae.";
Mol. Microbiol. 4:1303-1310(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.6%; Score 104; DB 1; Length 394; 76.2%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
T -> N (IN REF. 3).
W; 3F62C644A40E49DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00301; EFACTOR_GTP; 1.
Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFTU_MYCPN STANDARD; PRT; 394 AA. P23566; P75126; Created) 01-NOV-1991 (Rel. 30, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) TUF OR MPN665 OR MP177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-91125132; PubMed=2126326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004161; GTP_EFTU_2.
InterPro; IPR004161; GTP_EFTU_2.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
PRINTS; PR00315; ELONGAINECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; Pubmed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                EMBL, X16463; CAA34483.1; -.
EMBL; U39727; AAB01641.1; -.
EMBL; U39272; AAD12521.1; -.
EMBL; U02255; AAD12520.1; -.
PIR; S14909; EFYMTG.
HSSP; P02990; IETU.
TIGR; MG451; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000795; GTP_EFTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 REKFDRSKPHVNVGTIGHIDH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                       BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 36
EFTU_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
  <u>:</u>
  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

HV -> QL (IN REF. 1).

S -> I (IN REF. 1).

L -> V (IN REF. 1).

EWIPTPEREVOK -> DGFQLLNVKWTN (IN REF. 1).

E -> V (IN REF. 1).

T -> S (IN REF. 1).

T -> S (IN REF. 1).

E-> V (IN REF. 1).

E-> V (IN REF. 1).

E-> S (IN REF. 1).

EVLE -> KCLNSESRILSWLC (IN REF. 1).

EVLE -> KCLNSESRILSWLC (IN REF. 1).
"Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                    SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                      Nucleic Acids Res. 24:4420-4449(1996).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.6%; Score 104; DB 1; Length 394; 76.2%; Pred. No. 1.2e-09; ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X55768; CAA39292.1; -.

EMBL; AE000019; AAB95825.1; -.

FIR; S11997; S11997.

HSSP; P02990; LETU.

InterPro; IPR000795; GTP_EFTU.

InterPro; IPR004160; GTP_EFTU_D2.

InterPro; IPR004160; GTP_EFTU_D2.

Pfam; PF03144; GTP_EFTU_D2; 1.

Pfam; PF03144; GTP_EFTU_D2; 1.

Pfam; PR03143; GTP_EFTU_D2; 1.

PRNINTS; PR00315; ELONGATNFCT.

PROSITE; PS00301; ERACTOR_GTP; 1.

PROSITE; PS00301; ERACTOR_GTP; 1.

Elongation factor; Protein biosynthesis; GTP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
01-0CT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 REKFDRSKPHVNVGTIGHIDH 23
                                                                                                                                                                                                                                                        EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
85
139
139
112
122
122
209
209
360
394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
391
394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
NP_BIND 19
NP_BIND 81
NP_BIND 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 16; Conserv
```

```
STRAIN-MYX 2105;
MEDLINE=94368062; Pubmed=8085791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; CFB group; Taxeobacter.
NCBL_TaxID=36878;
                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                                                                                       2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                    3 KEKFNRTNPHVNIGTIGHVYH 23
                                                                                                                                                                                                                                                                                                                      84.6%;
90.5%;
                                                                                                                                                                                                                                                                                43730
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                          26
85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taxeobacter ocellatus
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                               399 AA;
                                                                                                                                                                                                                               Complete proteome.
NP_BIND 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFTU_TAXOC P42480;
                                                                                                                                                                                                                                                       NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 KESULT 39
EFTU_TAXOC
   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                     C -1- SUBUNIT: MONOMER (BY SIMILARITY).

C -1- SUBUNIT: MONOMER (BY SIMILARITY).

C -1- SUBCELLULAR LOCATION: CYtoplasmic.

C -1- SUBCELLULARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

ETTYLE-1A SUBFAMILY.

R PSSP; D05069; D60663.

R INCEPPC: IPR000795; GTP-EFTU.D2.

R INCEPPC: IPR004160; GTP-EFTU.D2.

R INCEPPC: IPR004160; GTP-EFTU.D2.

R Pfam; PF003144; GTP-EFTU.D2; 1.

R Pfam; PF03144; GTP-EFTU.D2; 1.

R Pfam; PF03144; GTP-EFTU.D2; 1.

R Pfam; PR03145; ELONGATNEFT:

R PROSITE; PR0315; ELONGATNEFT:

R PROSITE; PR00315; ELONGATNEFT:

R PLIND 19 26 GTP (BY SIMILARITY).

PR BIND 136 139 1 GTP (BY SIMILARITY).

PR PLIND 136 139 1 GTP (BY SIMILARITY).
              Leidel E., Lenz T., Ludvigsen A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBGNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY
--- EF-TU/ZE-1A SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
          Ludwig W., Welzenegger M., Betzl D., Leidel E., Lenz T., Ludvigser Moellenhoff D., Wenzig P., Schleifer K.H.; "Complete nucleotide sequences of seven eubacterial genes coding the elongation factor Tu: functional, structural and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q.
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                       Arch. Microbiol. 153:241-247(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-MINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                                                                  Score 104; DB 1; Length 39.
Pred. No. 1.2e-09;
2; Indels
                                                                                                                                                                                                                                                                                                                                          136 139 GTP (BY SIMILARITY).
396 AA; 42876 MW; EE21378647AFD644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
TUF OR TUFA OR JHP1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
MEDLINE=90240875; PubMed=2110445;
                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                             84.68;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOSYNTHESIS.
                                                                                                                 BIOSYNTHESIS.
                                                               evaluations."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFTU_HELPJ
                                                                                                                                                                                                                                                                                                                                           NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              092K19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
EFTU_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C., Klugbauer S., Reetz K., Schachtner I., Ludvigsen A., Bachleitner W., Fischer U., Schleifer K.H.; "Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLUAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antonie Van Leeuwenhoek 64:285-305(1993).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE001541; AAD06711.1; -...
HSSP; P02990; 1ETU.
InterPro; 1PR000416; GTP_EFTU.
InterPro; 1PR004160; GTP_EFTU.
InterPro; 1PR004160; GTP_EFTU_D2.
InterPro; 1PR004160; GTP_EFTU_D3.
InterPro; PF001049; GTP_EFTU_D3.
InterPro; PR00143; GTP_EFTU_D3.
InterPro; PR003145; GTP_EFTU_D3: 1...
InterPro; PR00315; EDONGATNECT.
InterPro; PR00310; EFACTOR_GTP; 1...
InterPro; PR00310; PR00310; EFACTOR_GTP; 1...
InterPro; PR00310; PR00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
4E72A877BFCD104B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 104; DB 1;
Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ludwig W., Neumaier J., Klugbauer N., Brockmann E., Roller C., Klugbauer S., Reetz K., Schachtner I., Ludwigsen A., Bachleitner M., Fischer U., Schleifer K.H.; "Phylogenetic relationships of Bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBUNIT: MONOMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antonie Van Leeuwenhoek 64:285-305(1993).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%; Score 103; DB 1; Length 395;
85.7%; Pred. No. 1.8e-09;
Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpetosiphon aurantiacus (Herpetosiphon giganteus).
Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
Herpetosiphon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                     Elongation factor; Protein biosynthesis; GTP-binding. NP_BIND 19 26 GTP (BY STWILARITY). NP_BIND 81 85 GTP (BY STMILARITY). GTP (BY STMILARITY). SEQUENCE 395 AA; 43038 MW; 168222411386D156 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Elongation factor Tu (EF-Tu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                     InterPro; IPR00095; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PR03143; GTP_EFTU_D2; 1.
PRINTS; PR00315; ELONGATNET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=HPGA1;
MEDLINE=94368062; PubMed=8085791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IRR000795; GTP_EFTU.
InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KEKFNRTKPHVNIGTIGHVDH 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X77036; CAA54325.1; -. HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X76868; CAA54196.1; -. HSSP; P02990; 1EFU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EF-TU/EF-1A SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.7
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFTU_HERAU
P42477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFTU_HERAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SY THE SY A SY THE SY THE SY A SY THE SY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

P45737 bacteroides P44390 haemophilus 097492 canis famil 064405 cavia porce			027710 onchocerca	068146 vibrio fisc 09w87 rattus norv	P07145 ipomoea bat	Q9xzd5 toxoplasma P48351 cucurbita p	P48352 cucurbita p Q9pwf7 rana rugosa	P49315 nicotiana p Q9xhh3 lycopersico	Q9y5s8 homo sapien P36625 schizosacch Q9axh0 avicennia m		P00432 bos taurus Q59602 neisseria g	ascaris					P31554 escherichia	P0///U acinetobact P55303 aspergillus	Q926x0 listeria in P24168 listeria se	P33569 streptomyce	910014 mycobacteri P78753 schizosacch	015296 homo sapien	09h115 homo sapien	US9337 deinococcus P94377 bacillus su	P34689 caenorhabdi 09v794 schizosacch	092405 aspergillus			V48/2 Salmonella O46522 b cytochrom	esch	O88/08 mus musculu P54571 bacillus su	s cytochr		P24597 mouse polyo P14726 hordeum vul				
1 CATA_BACFR 1 CATA_HAEIN 1 CATA_CANFA 1 CATA_CAVPO				CATA_VIBFI				CAT1_NICPL CAT2_LYCES				CATA_ASCSU					OSTA_ECOLI					LX1B_HUMAN		CATA_DEIRA				YACH			1 ORC4_MOUSE 1 YOKI BACSU		-			ALIGNMENTS		
526 1																																						
4.4.4.		4 4 4 6 6 8 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6	٠. م			8		99			9.0.0		ď.		34.4 34.4	4 <	 * - -	ກ ຕ	33.1			40			。。		. o	60	. o	9.0		6	γo,	00	;			
65 65 65 65	4 4 2	0 0 0 0 4 4 E E	62	61	09	29	0 0 0	58 58	58 57 75	57	57 56 87	រស	55	5 4 4 5 4 4	54 54	54	54	52.5	52	20	4. 4. V Q	4 9 8 8	4.	4 4 8 8	4 4 8 8	47.5	47	47	46.5	46.5	4 4 6 0	46	4 4 6 9	45.5)			1
4.5 Compugen Ltd.		earch time 13.53 Seconds (without alignments) 82.991 Million cell updates/sec		29				: 105224						cted by chance to have a of the result being printed, score distribution.			Description	• -	၎	,,,,	P18123 zea mays (m	P55308 hordeum vul	P55310 secale cere	P1/398 gossypium n P48350 cucurbita p	P25819 arabidopsis P55307 hordeum vul	P55313 triticum ae	Q92n99 desultovibr P32290 phaseolus a	methanosa		.,				×4 ×	glycine ma	P49317 nicotiana p O48560 glycine max	glycine max sus scrofa	hom
GenCore version 4.5 Copyright (c) 1993 - 2000 Comp	protein search, using sw model	August 22, 2002, 07:45:38 ; Search (with 82.99)	C-727-731	APVWDDNNVITAGPRG		BLOSUM62 Gapop 10.0 , Gapext 0.5	105224 seqs, 38719550 residues	f hits satisfying chosen parameters	length: 0 length: 2000000000	, , , , , , , , , , , , , , , , , , ,	<pre>j: Minimum Match 0% Maximum Match 100% Listing first 100 summaries</pre>	1 1	SWISSPIOL_40:*	 1s the number of results predisater than or equal to the score erived by analysis of the total 	SUMMARIES		Match Length DB ID	100.0 505 1 CATP	100.0 505 1 CATA 59.2 484 1 CATA	56.1 482 1	52.2 496 1	50.0 494 1	49.4 492 1	47.8 492 1	47.8 492 1 47.1 492 1	47.1 492 1	46.5 492 1	45.9 505 1	45.2 494 1	44.6 492 1	43.3 492 1 CATE	43.3 492 1	43.3 492 1 CATA	43.3 494 1 CATA 42.7 479 1 CATA	42.7 492 1 CATI	42.7 492 1 CAT3_ 42.7 492 1 CAT3_	42.0 502 1 CATA_	42.0 526 1
<u> </u>	OM protein – pr	Run on:	#i+]p.	Perfect score: Sequence:		scoring table:	Searched:	Total number of	Minimum DB seq	7	Post-processing	400 000 000 000		Pred. No. score gre and is de		Result	No. Score	1	7	ò	6	78	77													30 67		

~

```
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                           MEDLINE-97113460; PubMed-8955320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002226; Catalase.
Pfam; PF00109; Catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67458; AAC16068.1; -.
EMBL; Z70679; CAA94567.1; -.
EMBL; AE000597; AAD07923.1; -
HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                     Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
1129
339
339
234
237
248
255
286
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
ACT_SITE 56
ACT_SITE 129
BINDING 339
                                                                                                                                                                                               [3]
SEQUENCE FROM N.A.
                                     SEQUENCE FROM N.A.
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
129
339
339
234
237
237
248
255
313
                  NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; HP0875
                                                                                                                                  STRAIN-P1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                              pylori
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                MEDLINE=99120557; PubMed=9923682; Alm R.A. Ling L.S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria "Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                        "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
475A07EF6EF9B309 CRC64;
                                                                             Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00199; catalase; 1.
PRINTS: PR00067; CATALASE.
PRODOM: PD00510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1;
4.3e-16;
                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT, 505 AA. P77872; P94823; STANDARD; PRT; 505 AA. P77872; P94823; O1-NOV-1997 (Rel. 35, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O-CCT-2001 (Rel. 40, Last annotation update) Catalase (EC 1.11.1.6). KATA OR HP0875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 157; E
100.0%; Pred. No. 4.3
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001510; AAD06391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                             NCBI_TaxID=85963;
                                                                   KATA OR JHP0809
                                                                                                    Helicobacter
        CATA_HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
                  092KX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATA_HELPY
                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-i- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.
-i- COFACTOR: HEME GROUP.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-2 6695, ATCC 700392;
MEDLINE-36695, ATCC 700392;
MEDLINE-97394467; Pubmed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson K., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Wenter J.C.;
MEDIINE-98207782; PubMed=9546115;
Manos J., Kolesnikow T., Hazell S.L.;
"An investigation of the molecular basis of the spontaneous
occurrence of a catalase-negative phenotype in Helicobacter pylori.";
Helicobacter 3:28-38(1998).
                                                                                                                                                                                                                                                                                                                                                                                          Odenbreit S., Wieland B., Haas R.; "Cloning and genetic characterization of Helicobacter pylori catalase and construction of a catalase-deficient mutant strain."; J. Bacteriol. 178:6960-6967(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S -> F (IN REF. 1
Y -> I (IN REF. 2
Y -> H (IN REF. 2
N -> D (IN REF. 2
F -> Y (IN REF. 2
L -> T (IN REF. 2
A -> V (IN REF. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME I
```

```
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BP504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATA_ORYSA P29611;
                                                                                                                                                                CATA_BORPE
P48062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
BINDING
SEQUENCE
                                                                                                                              CATA_BORPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATA_ORYSA
                                       ŏ
                                                                       qq
                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERVES
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gouet P., Jouve H.-M., Dideberg O.; "Crystal structure of Proteus mirabilis PR catalase with and without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bound NaDPH.";

Lound NaDPH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OXYGEN; S
PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buzy A., Bracchi V., Sterjiades R., Chroboczek J., Thibault P., Gagnon J., Jouve H.-M., Hudry-Clergeon G., "Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a methionine sulfone in the close proximity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; P0000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                           ö
                                                                                                           Indels
                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 PROXIMAL HEME LIGANU.
55614 MW; ADC25F3CB41F5C50 CRC64;
 -> T (IN REF. 2).
9F029B55B73C26EA CRC64;
                                                                       Score 157; DB 1;
Pred. No. 4.3e-16;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHIONINE SULFONE.
                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                       484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                             29
                                                                                                                                                                PRT;
                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95305957; PubMed=7786407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95311317; PubMed=7791219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Protein Chem. 14:59-72(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 2CAE; 08-DEC-96.
PDB; 2CAF; 07-DEC-96.
PDB; 2CAG; 11-JAN-97.
InterPro; IFR002225; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00057; CATALASE.
   S
                                                                                                           ö
   316 s
58629 MW;
                                                                   100.08;
ilarity 100.08;
Conservative 0;
                                                                                                                                                                                                                                                                       STANDARD;
 316 3
505 AA;
                                                                 Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure
                                                                                                                                                                                                                                                                     CATA_PROMI
P42321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                     RESULT 3
CATA_PROMI
   SOF
                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                               a
```

Length 484;

Score 93; DB 1; Pred. No. 1.9e-06;

59.2%; 82.6%;

Best Local Similarity

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@liber.ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deshazer D., Wood G.E., Friedman R.L.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = O(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
;;
  ö
                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IFR00199; catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE; 1.
PROSITE; PS00437; CATALASE_1: 1.
PROSITE; PS00438; CATALASE_2: 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.1%; Score 88; DB 1; Length 482. 65.5%; Pred. No. 1.1e-05; Live 3; Mismatches 5; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROXIMAL HEME LIGAND (BY 7CB73E08975C219F CRC64;
    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Catalase isozyme A (EC 1.11.1.6) (CAT-A).
                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 AA
                                                                                                                                                                                                           482 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
    1;
                                                                                      27
                                             7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54508 MW;
                                                                          EMBL; U07800; AAA18481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
340
3482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF DA
```

```
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; c. InterPoly Catalase, a Pro199; catalase, a Pro199; catalase, a Pro199; catalase, a Pro199; catalase, a Pronom; PR00199; catalase, a Probom; PR001067; Catalase; 1. DR PROSITE; PS00435; CATALASE_1; 1. DR PROSITE; PS00438; CATALASE_1; 1. DR PROSITE; PS00438; CATALASE_1; 1. KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; catal catalase, a Catalase, and a Proximal Remains and a Proximal Remains and a Proximal Remains and a PROXIMAL HEME LIGAND (BY SIMILARITY).

PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                     Higo K., Higo H.;
"Cloning and characterization of the rice CatA catalase gene, a homologue of the maize Cat3 gene.";
Plant Mol. Biol. 30:505-521(1996).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                         -:- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP.
-:- SUBBUIT: HOMOTETRAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: PEROXISOMMAL and 91yoxysommal (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
          Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                Mori H., Higo K., Higo H., Minobe Y., Matsui H., Chiba S.; "Nucleotide and derived amino acid sequence of a catalase cDNA isolated from rice immature seeds."; Plant Mol. Biol. 18:973-976(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.2%; Score 83.5; DB 1; Length 491; 61.5%; Pred. No. 5.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 16, Created)
(Rel. 33, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                      STRAIN-CV. INDICA; TISSUE-Immature seed; MEDLINE-92256818; PubMed-1581574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                             STRAIN=CV. JAPONICA; TISSUE=Leaf; MEDLINE=96189265; PubMed~8605302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X61626; CAA43814.1; -.
EMBL; D29966; BAA06232.1; -.
PIR; S20873; CSRZ.
HSSP; P00432, 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                  PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAT3_MAIZE
P18123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAT3_MAIZE
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Blophys. Acta 951:104-116(1988).

I blophys. Acta 951:104-116(1988).

I blophys. Acta 951:104-116(1988).

I brothor. BECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE. ITS LEVELS ARE HIGHEST IN THE LIGHT PERIOD AND ARE LOWEST IN THE DARK PERIOD, HENCE MAY BE IMPORTANT FOR SCAVENGING HYDROGEN PEROXIDE AT NIGHT, THAN DURING THE DAY.

I COFACTOR: HENCE GROUP.

I SUBUNIT: HOMOTETRAMER.

I SUBUNIT: HOMOTETRAMER.

I TISSUE SPECIFICITY: LEAF MESOPHYLL CELLS, PERICARP, SEEDLING ROOTS AND THE COLEOPTILE.
                                                                       Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
-1- COUTION: THERE ARE TWO EMBL ENTRIES THAT CORRESPOND TO THE REF.2 SEQUENCE AND THEY ENCODE SLIGHTLY DIFFERENT PROTEINS (SEE THE FEATURE TABLE).
                                                                                                                                                                                                                                                                                                                                                                             "Isolation and characterization of a genomic sequence encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CV. W64A; TISSUE=Epicotyl;
MEDLINE=89051000; Pubmed=2461221;
Redinbaugh M.G. Wadsworth G.J., Scandallos J.G.;
"Characterization of catalase transcripts and their differential expression in maize.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROXIMAL HEME LICAND (BY SIMILA
A -> D (IN REF. 2).
C -> S (IN REF. 2).
T -> Q (IN REF. 2).
H -> P (IN REF. 2).
R -> P (IN REF. 2).
PE -> GR (IN REF. 2).
PE -> GR (IN REF. 2).
D -> H (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS, PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Mitochondrion; Multigene family.
01-FEB-1996 (Rel. 33, Last annotation update) Catalase isozyme 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                            STRAIN-CV. W64A; TISSUE-Seedling leaf; MEDLINE-94003062; PubMed-8400123;
                                                                                                                                                                                                                                                                                                                                                                                                              maize Cat3 catalase gene.";
Plant Mol. Biol. 22:1031-1038(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M33103; AAA33441.1; -.
EMBL; X12539; CAA31057.1; -
PIR; JA0091; JA0091.
HSSP; P00422; 4BLC.
MaizeDB; 13855; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L05934; AAC37357.1; -.
                                                                                                                                                                                                                                                                                                                                                     Abler M.L., Scandalios J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
140
157
107
110
1112
1116
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
351
57
79
110
1112
1112
1115
```

```
KATA OR PA4236.
                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                     STRAIN-FRD1
                                                                                                                                                                                                          CATA_PSEAE
                                    ACT_SITE
BINDING
                                                                                          Query Match
                                                          SEQUENCE
                                                                                                    Best Loca
Matches
                                                                                                                                                                                                CATA_PSEAE
     KW
KW
FT
FT
SO
                                                                                                                                   ò
                                                                                                                                                       셤
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN—CV MOREX;
MEDLINE—96145511; pubmed=8555444;
MEDLINE—96145511; pubmed=8555444;
MADLINE—96145511; pubmed=8555444;
MADLECULAR Clouing, characterization and expression analysis of two catalase isozyme genes in barley.";
Plant MAD. Biol. 29:1005-1014(1955).
-I- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP (BY SIMILARITY).
-i- SUBNIT: HOMOTETRAMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: PEROXISOME1 and 91yoxysome1 (By similarity).
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                       RRFADSLGHPKVSQ -> KAIRRLARTPQRQP (IN
                                                                                                                                                                                                            ö
V -> E (IN REF. 2).
C -> S (IN REF. 2; AAA3341).
AL -> R (IN REF. 2).
MISSING (IN REF. 2).
A -> AE (IN REF. 2).
DT -> AQ (IN REF. 2).
E -> Q (IN REF. 2).
F -> L (IN REF. 2).
AH -> G (IN REF. 2).
AH -> G (IN REF. 2).
                                                                                                  F -> L (IN REF. 2).
PLRQAAP -> RRCGRAA (IN REF. 2).
                                                                                                                                                                                    Score 82; DB 1; Length 496;
Pred. No. 9.2e-05;
2; Mismatches 5; Indels
                                                                                                                                                     566FFD05B3795B49 CRC64;
                                                                                                                                                                                                                                                                                                                            01-00T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                REF. 2).
C -> V (IN REF.
                                                                                                                                                                                                                                                                                                          494 AA
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                              Catalase 1sozyme 2 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSP; P00432; 4BLC.
interPro; IPR002226; Catalase.
                                                                                                                                                                                                                                          56796 MW;
                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                     52.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U20778; AAA96948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley).
                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                         STANDARD;
                        245
254
264
264
281
282
319
315
316
408
                                                                                                                                                       496 AA;
                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4513;
   2334
2234
2244
2254
2264
2282
3319
4402
452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEROXIDE.
                                                                                                                                                                                                                                                                                                         CAT2_HORVU
P55308;
   CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                     SEQUENCE
                                                                                                                                                                                      Query Match
                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                    RESULT 7
CAT2_HORVU
                                                                                                                                                                                                          Matches
    ò
                                                                                                                                                                                                                                                   a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 15692 / PAO1;
MEDLINE-2043737; PubMed-10984043;
MEDLINE-2043737; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.,W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ma J.-F., Ochsner U.A., Klotz M.G., Nanayakkara V.K., Howell M.L., Johnson Z., Posey J.E., Vasil M.L., Monaco J.J., Hassett D.J.; Bacterioferritin A modulates catalase A (KatA) activity and resistance to hydrogen peroxide in Pseudomonas aeruginosa."; J. Bacteriol. 181:3730-3742(1999).
                                                                                                                  PROXIMAL HEME LIGAND (BY SIMILARITY). 67E3CF2AD02E542E CRC64;
                                                                                                                                                                                                                                                                                               Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                    Length 494;
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                 50.0%; Score 78.5; DB 1;
ilarity 57.7%; Pred. No. 0.00031;
Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ź
                  Percoxisone; Glyoxysone; Multigene family.
ACT_SITE 65 65 BY SIMILARITY.
ACT SITE 138 138 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                       5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99296583; PubMed-10368148;
                                                                                                                                                                                                                                                                                                                                                                                                               13 DTKTTTTNAGOPVWNDNEALTVGPRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF047025; AAC03118.1; -. EMBL; AE004841; AAG07624.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                 56913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, La Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                          65
138
348
494 AA;
                                                                                                                                                                                                                                                                   Local Similarity
es 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 kDa PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
```

us-09-488-737-2.rsp

```
ACT_SITE
ACT_SITE
BINDING
                                                                                                                                                                                             RESULT 10
CAT1_GOSHI
                                                                                                                                   g
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
Trititoeae, Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

D725C042259AE494 CRC64;
                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                           ö
             Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD00510; Catalase; 1.
PROSITE; PS00433; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                   ; Db 1,
. 0.00036;
. 3 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PrNTS; PR00067; CATALASE.
ProDom; PD005107; CATALASE.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; FALSE_NEG.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                ch 49.7%; Score 78; DB 1; Length 482, I Similarity 57.1%; Pred. No. 0.00036; 16; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                         PROXIMAL HEME LIGAND (BY 8 84E5ABA647CAB414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
catalase (EC 1.11.16).
Secale cereale (Rye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA.
                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              2 VNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                 55 B)
128 B)
338 PI
55589 MW;
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. HALO; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z54143; CAA90858.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peroxisome; Glyoxysome
                                                                                                                                                                                                      482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347
492 AA;
                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 16; Conserv
                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                   55
128
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P42321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATA_SECCE
P55310;
                                                                                                                                                                   ACT_SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 FFFF WE WAR BRANK BRA
                                                                                                                                                                                                                                                                                                                                            õ
```

```
Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESPIRING ORGANISMS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gossypium hirsutum (Upland cotton).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-!- CORACTOR: HERE GROUP.
-!- SUBBURIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Peroxisomal.
-!- SUBCELLULAR LOCATION: PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
64886966A095F261 CRC64;
                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N. W., Turidy R.B., Trelease R.N.;
"Characterization of a CDNA encoding cottonseed catalase.";
Biochim. Biophys. Acta 1049:219-221990.
-i- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00432; 4BEC.

InterPro; IPR002226; Catalase.

Pfam; PF00199; catalase, 1.

PRINTS; PR00067; Catalase; 1.

ProDom; PD000510; Catalase; 1.

PROSITE; PS00437; CATALASE.

PROSITE; PS00437; CATALASE.2; 1.

Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Peroxisome; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.4%; Score 76; DB 1; Length 492; Best Local Similarity 61.9%; Pred. No. 0.00074; Matches 13; Conservative 4; Mismatches 4; Indels
                                                               Indels
   Score 77.5; DB 1;
Pred. No. 0.00044;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (Rel. 15, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                          492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. DELTAPINE 62; TISSUE-COLYledon;
MEDLINE-90304227; PubMed-2364113;
                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                  29
                                                                                                                                                    5 DVKQTTAF-GAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MΨ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X52135; CAA36380.1; -. PIR; S10770; S10770. PIR; S10395; S10395.
Query Match
Best Local Similarity 57.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56855
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAT1 OR SU1
                                                                                                                                                                                                                                                                                                                          CAT1_GOSHI
```

```
P25819; 049615;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                     pumpkin.";
Plant Mol. Biol. 33:141-155(1997).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
- SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                Cucurbita pepo (Vegetable marrow) (Summer squash).
Bukaryota, Viridiplantae; Streptophyta; Bmbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-!- COFACTOR: HEME GROUP (BY SIMILARITY).
-!- SUBUNIT: HOMOTERRAMER (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: G1YOXYSOMB1.
-!- TISSUE SPECIFICITY: HIGH EXPRESSION IN SEEDS AND EARLY SEEDLINGS.
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                 Esaka M., Yamada N., Kitabayashi M., Setoguchi Y., Tsugeki R., Kondo M., Nishimura M.; "CDNA cloning and differential gene expression of three catalases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROXIMAL HEME LIGAND (BY SIMILARITY). B02C649F767FAC20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOm; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Match 47.8%; Score 75; DB 1; Length 492; Local Similarity 61.9%; Pred. No. 0.001; es 13; Conservative 4; Mismatches 4; Indels
                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492 AA.
                                                                  492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                         MEDLINE-97188581; PubMed-9037166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 AA; 57070 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glyoxysome; Multigene family.
ACT_SITE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D55645; BAA09506.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                  STANDARD;
                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=3663;
                                                                                                                                                                                                                                                                                                                                   PEROXIDE.
                                                               CAT1_CUCPE
P48350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAT2_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
BINDING
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAT2_ARATH
                                                       CAT1_CUCPE
                                                                             ò
           ద
```

```
or 101-MAY-1997 (Red. 14, Last sequence update)

101-MAY-1997 (Red. 14, Last sequence update)

101-MAY-2002 (Red. 14, Last sequence update)

101-MAY-2002 (Red. 14, Last sequence update)

101-MAY-2002 (Red. 14, Last sequence update)

102 (Red. 101-MAY-2002)

103 (ATT OR CAT OR WAGGES)

104 (ATT OR CAT OR WAGGES)

105 (Remembrophyta; December of the control of the c
```

œ

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4565;
                                                               PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAT2_WHEAT
ID CAT2_WHEAT
AC P55313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
         SOUND DAY WENT WENT WAS A SOUND DAY OF THE SOUND DAY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                           SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROXIMAL HEME LIGAND (BY SIMILARITY).

I -> V (IN STRAIN CV. LANDSBERG ERECTA).
P -> L (IN REF. 1).
E -> A (IN REF. 1).
M -> I (IN REF. 1).
V -> L (IN REF. 1).
V -> L (IN REF. 1).
AB622230561FD79B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantãe; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                          -i-SUBUNIT: HOMOTETRAMER AND HETEROTETRAMER. AT LEAST SIX OR SEVEN ISOZYMES ARE PRODUCED FROM A MIXTURE OF 3 GENE PRODUCTS.
-i-SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal.
-i-SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. MOREX;
MEDLINE=96145511; PubMed=8555444;
Skadsen R.W., Schulze-Lefert P., Herbst J.M.;
Molecular cloning, characterization and expression analysis of two catalase isozyme genes in barley.";
Nature 402:769-777(1999).

-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WAIER AND OXYGEN; S
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                   Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 1;
Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATI_HORVU STANDARD; F P55307; Q43761; O1-0CT-1996 (Rel. 34, Last sequisidance) 15-JUL-1998 (Rel. 36, Last annuments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                      EMBL; X64271; CAA45564.1; -. EMBL; X94447; CAA64220.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare (Barley).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
138
348
421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39
109
154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAT1_HORVU
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

Ŷ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Plant Mol. Biol. 29:1005-1014(1995).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                        -!- COFACTOR: HEME GROUP (BY SIMILARITY).
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-!- TISSUE SPECIFICITY: IN WHOLE ENDOSPERMS (ALEURONES PLUS STARCHY ENDOSPERM), IN ISOLATED ALEURONES AND IN DEVELOPING SEEDS.
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Song Z., Zhu Y., Hulliu G.J.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMAST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: HEME GROUP.
SUBUNIT: HOWOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROXIMAL HEME LIGAND (BY SIMILARITY). 5917F285FD75D725 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P004 212 * pbb.

InterPro: JPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1: 1.
PROSITE; PS00438; CATALASE_1: 1.
PROSITE; PS00438; CATALASE_1: 1.
PROSITE; PS00438; CATALASE_1: 1.
PROSITE: PS00438; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 2 \text{ H}(2)\text{O}(2) = \text{O}(2) + 2 \text{ H}(2)\text{O}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74; DB 1;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 348 F
492 AA; 56586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 TINSGAPVWNNNALTVGHRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.18;
61.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U20777; AAA96947.1; -. EMBL; U16132; AAA62306.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATA.
Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
```

us-09-488-737-2.rsp

Hydrogen peroxide

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN, SERVES
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

CFARD23345E03C94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitamura M., Kojima S., Akutsu H., Kumagai I., Nakaya T.;
Gatalase from strictly anaerobic bacteria, Desulfovibrio vulgaris
(Miyazaki F).";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                              HSSP; P00432; 4BLC.
InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase.
PRINTS; PR00109; Catalase; 1.
PRINTS; PR000510; Catalase; 1.
PROSITE; PS00437; CATALASE.
PROSITE; PS00438; CATALASE...; 1.
PROSITE; PS00438; CATALASE...; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desulfovibrio vulgaris (strain Miyazaki).
Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 74; DB 1;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
80-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
Prodom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                           138 138 B
348 348 P
492 AA; 56480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB020341; BAA34670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P42321; 2CAE.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TINSGAPVWNNNALTVGHRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                     47.18;
61.98;
                                                                                                                                             EMBL; X94352; CAA64077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                          Peroxisome; Glyoxysome.
ACT_SITE 65 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATA_DESVM
Q92N99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KATA OR KAT
                                                                                                                                                                                                                                                                                                                                           ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
CATA_DESVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phaseolus aureus (Mung bean) (Vigna radiata).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
933E604D2611CE85 CRC64;
                                         SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-94151449; PubMed-8108520;
Mori H., Imaseki H.;
"cDNA for catalase from etiolated mung bean (Vigna radiata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73; DB 1; Length 492;
Pred. No. 0.0021;
                                                                                           46.5%; Score 73; DB 1; Length 479;
65.2%; Pred. No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                       6; Indels
                                       PROXIMAL HEME LIGAND (BY 4CD97480AB6FD475 CRC64;
                                                                                                                                                                                                                                                                    01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
            BY SIMILARITY
BY SIMILARITY
                                                                                                                       2; Mismatches
Oxidoreductase; Peroxidase; Iron; Heme;
ACT_SITE 54 54 BY SIMILARI
ACT_SITE 127 BY SIMILARI
BINDING 337 337 PROXIMAL HE
SEQUENCE 479 AA; 54549 MW; 4CD97480A
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                  7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.5%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D13557; BAA02755.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity billing
Line 13; Conservative
                                                                                             Query Match 46.5
Best Local Similarity 65.2
Matches 15; Conservative
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
138
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peroxisome; Glyoxysome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00432;
                                                                                                                                                                                                                     RESULT 16
CATA_PHAAU
ID CATA_PHAAU
AC P32290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
    SFFFS
                                                                                                                                                     ò
```

g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OXYGEN; SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                          STRAIN=168 / YB886;
MEDLINE=92097949; PubMed=1756979;
Bol D.K., Yasbin R.E.;
"The isolation, cloning and identification of a vegetative catalase gene from Bacillus subtilis.";
Gene 109:31-37(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- DEVELOPMENTAL STAGE: ELEVATED LEVELS OF EXPRESSION DURING ENTRY INTO THE STATIONARY PHASE OF THE GROWTH CYCLE.
-i- INDUCTION: BY HYDROGEN PEROXIDE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-188.

SEQUENCE OF 1-188.

MEDLINE=94236234; PubMed=8180695;

Hartford O.M., Dowds B.C.A.;

Hartford O.M., Dowds B.C.A.;

Hartford Down and characterization of a hydrogen peroxide resistant mutant of Bacillus subtilis.";

Microbiology 140:297-304(1994).

-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; S TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-!- CAPALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

-!- COFACTOR: HEME GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R EMBL; M80796; AAA22402.1; -.
R EMBL; Z82044; CAB04807.1; -.
R EMBL; Z99108; CAB12710.1; -.
R PIR; JH0532; JH0532.
R HSSP; P00432; 4BLC.
R Subfilist; BG10849; katA.
R InterPro; IPR002226; Catalase.
R PRINTS; PR00067; CATALASE.
R PRODOM; P0000510; Catalase; 1.
R PROSITE; PS00437; CATALASE.
R PROSITE; PS00437; CATALASE.
R PROSITE; PS00438; CATALASE.2; 1.
R PROSITE; PS00438; CATALASE.2; 1.
R PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                    Cummings N.J., Connerton I.F.; "The Bacillus subtilis 168 chromosome from sspE to katA."; Microbiology 143:1855-1859(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.2%; Score 71; DB 1; Length 482; 60.9%; Pred. No. 0.0041; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 G -> P (IN REF. 1).
372 G -> D (IN REF. 1).
54602 MW; 749F7C88CEA2E047 CRC64;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                   Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                  MEDLINE=97346037; PubMed-9202460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KOTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _ _ _ _ _ _ _ _ _ _ _ _ _ _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.2
Best Local Similarity 60.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
53
126
336
205
372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
INIT_MET 0
ACT_SITE 53
ACT_SITE 126 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 AA;
                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 1-18
                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                  STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROXIMAL HEME LIGAND (BY SIMILARITY).
2A27C4BEC47BE854 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanosarcinales; Methanosarcinaceae;
                                                                                                                                                                                                                                                                                                                                                         STRAIN=FUSARO / DSM 804;
Shima S., Netrusov A., Sordel M., Wicke M., Hartmann G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P04040; 100W.

InterPro; IPR002256; Catalase.
Pfan, PF00199; catalase; 1.
PRINTS; PR00067; Catalase; 1.
PROSTIE; PS00437; Catalase; 1.
PROSTIE; PS00438; Catalase; 1.
PROSTIE; PS00438; Catalase; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%; Score 72; DB 1; Length 505;
66.7%; Pred. No. 0.0031;
Live 1; Mismatches 6; Indels
                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETS BACSU STANDARD; PRT; 482 AA. P26901; P77838; 01-AUG-1992 (Rel. 23, Created) D-EMC-1998 (Rel. 37, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Vegetative catalase (EC 1.11.1.6). Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
BY SIMILARITY
                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ005939; CAA06774.1; -.
57065 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.73
Matches 14; Conservative
                                                                                                              STANDARD;
                                                                                                                                                                                                                                              Methanosarcina barkeri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 3
505 AA;
                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2208;
                                                                                                                                                                                                                                                                                  Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                 Thauer R.K.;
                                                                                                            CATA_METBA
093662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESULT 18
CATA_BACSU
                                                                                          CATA_METBA
               18
```

ò 셤 SORPT

Gaps

ö

Indels

ر ري

Mismatches

5;

```
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                       RESULT 20
CAT1_MAIZE
Matches
                                                                δ
                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMEDLINE=21396507; PubMed=11481430;

A MEDLINE=21396507; PubMed=11481430;

A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

B Oistard P., Becker A., Boutry M., Cadiou E., Dreamo S., Gloux S.,

A Godite T., Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D.,

A Renard C., Thebault P., Vandenbol M., Weidher S., Galibert F.;

A Renard C., Thebault P., Vandenbol M., Weidher S., Galibert F.;

A Ralysis of the chromosome sequence of the legume symbiont

Sinorhizoblum meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 99:9877-9882(2001).

C I- FONCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES

C I- CATALYTIC ACTIVITY: 2 H(2)0(2) - 0(2) + 2 H(2)0.

C COCACTOR: HEME GROUP.

C I- SUBCELLULAR LOCATION: Periplasmic.

C I- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTDRPITTTAGAPVPDNQ -> MPPPLPERRHLICACVGT
YCGCGSNPPSGSSPFVPASFFVPAEGTAEPRCGGVSSPRSR
AGFSPRIRALISSPVSVSYSSKPSARAT (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herowart D., Sigaud S., Moreau S., Frendo P., Towati D., Puppo A.; "Cloning and characterization of the katA gene of Rhizobium meliloti encoding a hydrogen peroxide-inducible catalase."; J. Bacteriol. 178:6802-6809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROXIMAL HEME LIGAND (BY SIMILARITY)
                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase A (EC 1.11.1.6).
CATALASE A REC 1.11.1.6).
RATA OR ROU764 OR SMC00819.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00448; CATALASE_1; FALSE_NEG.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39FA86606D2D83D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMITA
                                                                                                                                                              494 AA
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-RCR2011 / SU47;
MEDLINE-97113440; PubMed-8955300;
KLTTSWGAPVGDNQNSMTAGSRG 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56008 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL591784; CAC45336.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Sinorhizobium
NCBI_TaxID-382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U59271; AAC44649.1;
                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P42321; 2CAE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Periplasmic;
                                                                                                                                                       CATA_RHIME P95631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
셤
                                                                                                                                                                                            SOTT THE TELL TO DESCRIBE TO THE PROPERTY OF T
```

Length 494;

Score 71; DB 1; Pred. No. 0.0042;

45.2%;

Best Local Similarity

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OXYGEN; SERVES PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY. PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. W648; TISSUE-Leaf; WEDLINE-94035156; PubMed-8220459; Guan L., Scandallos J.G.; PubMed-8220459; Guan L., Scandallos J.G.; Action L., Scandallos the catalase antioxidant defense gene Catl of maize, and its developmentally regulated expression in transgenic
                                                                                                                                                                                                                                                                                             STRAIN-CV. R6-67; TISSUE-Scutellum;
MEDLINE-89051000; PubMed-2461221;
Redinbaugh M.G., Wadsworth G.J., Scandalios J.G.;
"Characterization of catalase transcripts and their differential
expression in maize.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PROSTIE; PS00437; CATALASE_1; 1.
PROSTIE; PS00438; CATALASE_1; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
Peroxisome; Multigene_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> V (IN STRAIN W64A)
                                                                                                                        01-NoV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
Catalase isozyme 1 (EC 1.11.1.6).
                                                                                               492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                       expression in maize.";
Biochim. Biophys. Acta 951:104-116(1988).
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002226; Catalase.
9 TTAFGAPVWDDNNVITAGPRG 29
                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X12538; CAA31056.1; -. EMBL; X60135; CAA42720.1; -. PIR; JA0090; JA0090. HSSP; P21179; 1CF9. MaizeDB; 13855; --
              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
138
348
157
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=4577;
                                                                                                                                                                                                Zea mays (Maize)
                                                                                               CAT1_MAIZE
P18122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tobacco."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
```

Pred. No. 0.0059;

```
Best Local Similarity
                                                                                               RESULT 22
CAT1_ARATH
             Matches
                                                             셤
                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROXIMAL HEME LIGAND (BY SIMILARITY). 08963B05BA6C20AB CRC64;
                                                                                                                                    ;
0
                                                                                                            Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                    Indels
S -> T (IN STRAIN W64A).
P -> I (IN STRAIN W64A).
P -> A (IN STRAIN W64A).
A -> G (IN REF. 1).
C -> G (IN REF. 1).
C -> D (IN REF. 1).
C -> D (IN REF. 1).
                                                                                                           44.6%; Score 70; DB 1;
57.1%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
Catalase isozyme B (EC 1.11.1.6) (ART-B).
                                                                                                                                                                                                                                             492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase, controlled and a peroxisome; Multigene family.

ACT_SITE 65 BY SIMILARITY.

ACT SITE 138 138 BY SIMILARITY.
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                    ٠.
                                                                         Œ.
                                                                                                                                                           9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                         56519 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D26484; BAA05494.1; -. HSSP; P21179; 1CF9.
                                                                         56877
                                                                                                                                    Conservative
                                                                                                                                                                                                                                              STANDARD;
 211
329
483
332
415
                                                                                                           Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          492 AA;
                                                                         492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4530;
                                                                                                                                                                                                                                             CATB_ORYSA
                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
VARIANT
VARIANT
                                                                       SEQUENCE
                         VARIANT
                                                                                                                                                                                                                     RESULT 21
CATB_ORYSA
 ELLLLS
                                                                                                                                                            ò
```

Length 492;

DB 1;

44.6%; Score 70;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISMS AND
                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r,
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP.
-i- SUBUNIT: HOMOTETRAMER AND HETEROTETRAMER. AT LEAST SIX OR SEVEN
ISOZYMES ARE PRODUCED FROM A MIXTURE OF 3 GENE PRODUCTS.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. Columbia;
MEDLINE-98250696; PubMed=9584109;
MEDLINE-98250696; PubMed=9584109;
Firugoli J.A., McPeek M.A., Thomas T.L., McClung C.R.;
Genetics 149:355-365(1998).
                                                                                                                                                                                                                                                                                                                                                                                             Frugoli J.A., Zhong H.H., Nuccio M.L., McCourt P., McPeek M.A., Thomas T.L., McClung C.R.; Cartalase is encoded by a multigene family in Arabidopsis thaliana (L.) Heynh.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

G -> E (IN REF. 1).

G -> F (IN REF. 1).
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGAN SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
5
                                                                                                                                                                             ..... 41, Last sequence update) u1-MAR-2002 (Rel. 41, Last annotation update) catalase 1 (EC 1.11.1.6).
 Mismatches
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG ERECTA;
MEDLINE-96416445; Pubmed-8819328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 112:327-336(1996)
                                                                                                                                          CAT1_ARATH STANDARD; F 096528; 022529; 01-NOV-1997 (Rel. 35, Created) 01-MAR-2002 (Rel. 41, Last seq
                                                 18 TTNSGAPVWNNNSALTVGERG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF021937; AAC17731.1;
                               9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U43340; AAB07026.1;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEROXIDE.
```

```
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                 CONFLICT
                                                                                                                   CONFLICT
                                                                       CONFLICT
                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                            P30567
                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                            KKW
KKW
KKW
KT
FT
FT
FT
FT
SO
                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glyoxysomal targeting sequence.";
Eur. J. BLOchem. 199:121-215(1991).
-!- EUNCTION: OCCURS IN ALMOST ALLA BEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLE FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP.
-:- SUBCELLULAR LOCATION: Peroxisomal and glyoxysomal (Potential).
-:- TISSUE SPECIFICITY: ABUNDANT IN ENDOSPERMS AND COTYLEDONS. ONLY IN SMALL AMOUNT IN ROOT.
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                         TISSUE-Hypocotyl;
MEDLINE-94325474; PubMed-8049373;
Suzuki M., Ario T., Hattori T., Nakamura K., Asahi T.;
Suzuki M., Ario T., Hattori T., Nakamura K., Asahi T.;
Isolation and characterization of two tightly linked catalase genes from castor bean that are differentially regulated.";
                                                                                    Gaps
                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The C-terminal domain of plant catalases. Implications for
                                                           Length 492;
                                                                                  5; Indels
 L -> NV (IN REF. 1).
-> W (IN REF. 1).
370F54FF7D757C9B CRC64;
                                                          DB 1;
0.012;
                                                                                                                                                                                                             (Rel. 33, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                          492 AA
                                                                                  Mismatches
                                                          Score 68;
Pred. No.
  KL -> S
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 25:507-516(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. HALE;
MEDLINE=91293125; PubMed=1712298;
                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last annota
Catalase isozyme 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR002226; Catalase.
Pfam: PF00199; catalase; 1.
PRINKE: PR00067; CATALASE.
PRODOM: PD000510; Catalase; 1.
PROSITE: PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                           Ricinus communis (Castor bean).
                                                                                  4;
                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                      56861 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 404-492 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D21161; BAA04697.1; -. EMBL; X59694; CAA42215.1; -.
                                                        tch 43.3%;
al Similarity 57.1%;
12; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S16231; S16231.
PIR; S29333; S29333.
HSSP; P21179; 1CF9.
339 3
455 4
492 AA;
                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3988;
                                                                                                                                                                                                             01-FEB-1993 (
01-FEB-1996 (
01-FEB-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonzalez E.
                                                                                                                                                                                          CAT1_RICCO
CONFLICT
CONFLICT
SEQUENCE
                                                            Query Match
                                                                                 Matches
                                                                                                                                                                  SULT 23
                                                                                                                               18
                                                                                                                                                                                                    SFF
                                                                                                          ò
                                                                                                                               g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@liberity.).
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
VGBI_TaxID=3635;
                                                                                                                                                                                                                                                                                                                             Gaps
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
Peroxisome; Glyoxysome; Multigene family.
ACT_SITE 65 65 BY SIMILARITY.
ACT_SITE 138 138 BY SIMILARITY.
BINDING 348 348 PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                   Score 68; DB 1; Length 492;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                        B5E28A425088BF63 CRC64;
                                                                                                                      A -> P (IN REF. 2).
F -> S (IN REF. 2).
L -> F (IN REF. 2).
D -> E (IN REF. 2).
H -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA.
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. DELTAPINE 62; TISSUE-COtyledon;
MEDLINE-91378551; PubMed-1898069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catalase isozyme 2 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRODOG7; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSTTE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                               4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                            ..
Μ.
                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                        18 TINSGAPVWNNNSSLTVGSRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56675; CAA39998.1; -. PIR; S17493; S17493.
                                                                                                                                                                                                                            56464
                                                                                                                                                                                                                                                                                     Query Match 43.3
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                              138
444
4439
454
61
                                                             655 138 348 446 456 456 456 461 A89 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00432; 4BLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAT2 OR SU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
CAT2_GOSHI
ID CAT2_GOSHI
```

```
TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATA_PSEPU
Q59714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peroxisome
                                                                      CATA_PEA
P25890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATA_PSEPU
                                                                          WHITH EXECUTION OF THE PROPERTY AND THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                              BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
589FD8DCA1/3AB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Primulaceae; Soldanella.
NCBI_TaxID=66308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                               ö
                                                                                                                         Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.3%; Score 68; DB 1; Length 492; 57.1%; Pred. No. 0.012;
                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
PROXIMAL HEME LIGAND (BY 5
0CC8A9B2597A9EEA CRC64;
                                                                                                                         43.3%; Score 68; DB 1; 57.1%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                           01-WAR-2002 (Rel. 41, Created)
01-WAR-2002 (Rel. 41, Last sequence update)
01-WAR-2002 (Rel. 41, Last annotation update)
Catalase (EC 1.11.1.6).
Soldanella alpina (Alpine snowbell).
                                                                                                                                                                                                                                                                                                                               492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                               Mismatches
                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002226; Catalase.
Ffam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00431; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Oxidoreductase; Peroxidase, Iron;
                   ΒŸ
                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                      56935 MW;
                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                      56921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 TINSGAPVWNNNSSLIVGTRG 38
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z99633; CAB16749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
                 65
138
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
                 65
138
348
348
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
138
348
492 AA;
                                                                                                                                            1 Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Leaf;
 Peroxisome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peroxisome.
                                                                                                                                                                                                                                                                                                                             CATA_SOLAP
                 ACT_SITE
ACT_SITE
BINDING
                                                                      SEQUENCE
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                            CATA_SOLAP
                                                                                                                                                                                                                                    18
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
WIFF S
                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

g

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                    ISIN S.H., Allen R.D.;
"Isolation and characterization of a pea catalase cDNA.";
Plant Mol. Biol. 17:1263-1265(1991).
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                      Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X60169; CAA42736.1; -.
PIR; S18346; CSPM.
HSSP; P00432; 4BLC.
Interpro; PTR002226; Catalase.
Pfam; PR00199; catalase, 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00433; CATALASE_1; 1.
PROSITE; PS00433; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROXIMAL HEME LIGAND (BY B5FC08E66B13B266 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O. COFACTOR: HEME GROUP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBUNIT: HOMOTETRAMER.
-1- SUBCELLULAR LOCATION: Peroxisomal.
-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.3%; Score 68; DB 1;
ilarity 57.1%; Pred. No. 0.012;
Conservative 4; Mismatches
                                             01-MAY 1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Catalase (EC 1.11.1.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
494 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92032793; PubMed=1932700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 BY
138 BY
348 PF
57344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TINSGAPVWNNNSSLIVGSRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
138
348
494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          024448
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@illo.ch).
                                             SEQUENCE FROM N.A.
STRAIN=CV. CORSOY 79;
Su H., Hardy K.A., Hermsmeier D., Baum T.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
slbmitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: OCCURE IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                               -!- COFACTOR: HEME GROUP.
-!- SUBUNIT: HOWOTETRAMER.
-!- SUBCELLULAR LOCATION: PELOXISOMAl and glyoxysomal (By similarity).
-!- SUBILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Flower;
MEDLINE=95010681; PubMed=7925949;
Willekens H., Villarroel R., van Montagu M., Inze D., van Camp W.;
"Molecular identification of catalases from Nicotiana plumbaginifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROXIMAL HEME LIGAND (BY SIMILARITY).
CE8AFE8BEEA483C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBI_TaxID=4092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.7%; Score 67; DB 1; Length 492; 52.4%; Pred. No. 0.017; ive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                         -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Catalase isozyme 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; reloximos, legene family.
Peroxisome; Glyoxysome; Multigene family.
65 BY SIMILARITY.
7.7. 7.7. 7.7. 138 BY SIMILARITY.
Plant Mol. Biol. 17:1263-1265(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.; 1.
PROSITE; PS00438; CATALASE.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035252; AAB88169.1; -. EMBL; AF035253; AAB88170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56847 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1| |||:|::|: || |||
18 TINSGAPIWNNNSSLIVGSRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z12021; CAA78056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 352:79-83(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 42.7
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 1
348 3
492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S20999; CSSY.
HSSP; P21179; 1CF9
                                                                                                                                                                                    PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAT3_NICPL
ID CAT3_NICPL
AC P49317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
       Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                         putida.";
Gene 199:219-224(1997).
-!- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROXIMAL HEME LIGAND (BY SIMILARITY).
EFE3CBDE67778571 CRC64;
                                                                                                                                                                                                         Kim Y.C., Miller C.D., Anderson A.J.;
"Identification of adjacent genes encoding the major catalase and
bacterioferritin from the plant-beneficial bacterium Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                       Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.7%; Score 67; DB 1; Length 479; llarity 66.7%; Pred. No. 0.016; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. D&PL 415;
MEDLINE-92032793 bubmed=1932700;
Isin S.H., Allen R.D.;
"Isolation and characterization of a pea catalase cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide
                                                                                                                                                                                                                                                                                                                                                                                       -i- COFACTOR: HEME GROUP.
-i- ENZYME REGULATION: ACTIVATED BY PEROXIDE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
CATI AND CAT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                    MEDLINE-98019091; PubMed-9358059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE.1; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U63511; AAB88219.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                 STRAIN-CORVALLIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-3847;
                                                                                            NCBI_TaxID=303;
    OR CATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAT1_SOYBN P29756;
                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAT1_SOYBN
```

g

ò

ö

Gaps

```
PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CAT4_SOYBN 048561;
                                                                                                                                                                                                                                                                                                                                                                                                                     SOYBN
                                                                                                                                                                                                                                                                                                              Matches
     δλ
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
CATALTITC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
COFACTOR: HEME GROUP.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: PETOXISOMAL (POtential).
INDUCTION: BY 3-AMINOTRIAZOLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. CORSON 79;
SU H., Hardy K.A., Hermsmeier D., Baum T.J.;
Su H., Hardy K.A., Hermsmeier D., Baum T.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- CATALITIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-1- CORPACTOR: HEME GROUP.
-1- SUBGNIT: HOMOTETRAMER (By similarity).
-1- SUBGELLULAR LOCATION: Peroxisomal and glyoxysomal (By similarity).
-1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                         PROXIMAL HEME LIGAND (BY SIMILARITY).
2A49AD89CC6FB4D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                InterPro: 1PR00225; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; Peroxisome; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                            -!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67; DB 1;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase 3 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA
                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                      492 AA; 57016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TTNSGAPVWNNNSSMTVGTRG 38
                                                                                                                                                                                                                           EMBL; Z36977; CAA85426.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 42.7%;
1 Similarity 57.1%;
12; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAT3_SOYBN
048560;
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAT3_SOYBN
  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
A EMBL, AF035254; AAbou--
R HSPP; P21179; 1CF9.
A HSPO00510; Catalase; 1.
B PROSITE; PS00439; CATALASE.; 1.
B PROSITE; PS00439; CATALASE.; 1.
B PROSITE; PS00439; CATALASE.; 1.
B NOSITE; PS00439; CATALASE.; 1.
B NOSITE PS00439; CATALASE.; 1.
B NOSITE PS00439; CATAL
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. COISOY 79;
Su H., Hardy K.A., Hermsmeier D., Baum T.J.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALLA BEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-i- COFACTOR: HEME GROUP.
-i- SUBUNIT: HOMOTETRAMER (By similarity).
-i- SUBCELLULAR LOCATION: PEROXISOMEL and glyoxysomel (By similarity).
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max (Soybean).

Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Catalase 4 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002226; Catalase.
Pfam: PF00199; catalase; 1.
PRINES: PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF035255; AAB88172.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3847;
```

Gaps

ö

STTTS

ð 셤

```
X-RAY CRYSTALLOGRAPHY (2.75 ANGSTROMS).
MEDLINE-20133173; Pubmed-10666617;
KO T.P., Safo M.K., Musayev F.N., Di Salvo M.L., Wang C., Wu S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
MEDINE-20124014; PubMed-10656833;
Putnam C.D., Arvai A.S., Bourne Y., Tainer J.A.;
"Active and inhibited human catalase structures: ligand and NADPH
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korneluk R.G., Quan F., Lewis W.H., Guise K.S., Willard H.F., Holmes M.T., Gravel R.A.; Isolation of human fibroblast catalase CDNA clones. Sequence of clones derived from spliced and unspliced mRNA."; J. Biol. Chem. 259:13819-13823(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-21 FROM N.A. MEDILIBE-9110338; PubMed-9282800; MEDILIBE-9110338; PubMed-9282800; Voo J.-H., Erzurum S.C., Hay J.G., Lemarchand P., Crystal R.G.; "Vulnerability of the human airway epithelium to hyperoxia. Constitutive expression of the catalase gene in human bronchial epithelial cells despite oxidant stress."; J. Clin. Invest. 93:297-302(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDDLINE-8628646; PubMed-3755225;
Quan F., Korneluk R.G., Tropak M.B., Gravel R.A.;
"Isolation and characterization of the human catalase gene.";
Nucleic Acids Res. 14:5321-5335(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bell G.I., Najarian R.C., Mullenbach G.T., Hallewell R.A.; "cDNA sequence coding for human kidney catalase."; Nucleic Acids Res. 14:5561-5562(1986).
  Length 502,
                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
    DB 1;
0.024;
                                                                                                                                                                                                                                                                         01-NOV-1986 (Rel. 03, Created)
16-077-2001 (Rel. 40, Last sequence update)
18-1-1-2002 (Rel. 41, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abraham D.J.;
"Structure of human erythrocyte catalase.";
Acta Crystallogr. D 56:241-245(2000).
                                                                                                                                                                                                                                    526 AA
                                              Mismatches
    Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE-21065390; Pubmed=11134921;
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding and catalytic mechanism."; J. Mol. Biol. 296:295-309(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Fibroblast;
MEDLINE-85054813; PubMed-6548744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86286565; PubMed-375556;
                                           ٠.
ش
                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                             || | |: | |::||||||
TTGSGNPIGDKLNILTAGPRG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 76-526 FROM N.A.
    42.08;
                        57.1%;
  Query Match 42.0
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                CATA_HUMAN
ID CATA_HUMAN
                                                                                                                                                                                                                                                          P04040;
                                                                                                                             27
                                                                                                                             g
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-LANDRACE; TISSUE-Liver;
MEDINE-9913641; PubMed-947594;
Lin Z.-H., Wang Y.-F., Sarai A., Yasue H.;
Lin Z.-H., Wang Y.-F., Sarai A., Yasue H.;
Swine catalase deduced from cDNA and localization of the catalase
gene on swine chromosome 2p16-p15.";
Biochem. Genet. 35:297:302(1997).
-!- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
F40066EB3C424212 CRC64;
                                                                                                         PROXIMAL HEME LIGAND (BY SIMILARITY).
FEF3B4706A4FD669 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00432; 4BLC.
InterPro: IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODICM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                    42.7%; Score 67; DB 1; Length 492;
llarity 52.4%; Pred. No. 0.017;
Conservative 5; Mismatches 5; Indels
                          Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- CATALTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-- COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
-- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-- SUBCELLIARN LOCATION: PETOXISOMA! (By similarity).
-- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydl
Peroxisome; Glyoxysome; Multigene family.
ACT_SITE 65 BK SIMILARITY.
ACT_SITE 138 138 BK SIMILARITY.
BINDING 348 348 PROXIMAL HEME 1
                                                                                                                                                                                                                                                                                                                                                                                                                             502 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57182 MW;
                                                                                                                             492 AA; 56737 MW;
                                                                                                                                                                                                                                                                              TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                    18 TINSGAPIWNNNSSLTVGARG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D89812; BAA25301.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
74
147
357
502 AA;
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEROXIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peroxisome.
INIT_MET
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                           CATA_PIG
O62839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
BINDING
SEQUENCE
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                           CATA_PIG
```

```
ACT_SITE
ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
              a
                                                                      Dρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Safo M.K., Musayev F.N., Wu S.H., Abraham D.J., KO T.P.;
"Structure of tetragonal crystals of human erythrocyte catalase.";
Acta Crystallogr. D 57:1-7(2001).
-!- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                -: CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-:- COFACTOR: HEME GROUP AND NADP.
-:- SUBUNIT: HOMOTETRAMER.
-:- SUBCLILIA: HOMOTETRAMER.
-:- SUBCLILIA: LOCATION: Peroxisomal.
-:- DISEASE: Deficiency in CAT causes acatalasia (or acatalasemia).
This disease is charactelized by absence of catalase activity in red cells and is often associated with ulcerating oral lesions.
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROXIMAL HEME LIGAND.
7CA11394D124F6FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                               , X04092; CAA27721.1; JOINED.

; X04093; CAA27721.1; JOINED.

; X04095; CAA27721.1; JOINED.

; X04095; CAA27721.1; JOINED.

; X04096; CAA27721.1; JOINED.

; L13609; AAA16651.1;
                                                                                                                                                                                                                                                                                                 X04085; CAA27721.1; -
X04086; CAA27721.1; JOINED.
X04087; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                              X04089; CAA27721.1; JOINED. X04090; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                     X04091; CAA27721.1; JOINED. X04092; CAA27721.1; JOINED.
                                                                                                                                                                                                                                                                                                                                     X04088; CAA27721.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1F4J; 17-JAN-01.
SWISS-2DPAGE; P04040; HUMAN.
Aarhus/Ghent-2DPAGE; 1524; IEF.
Aarhus/Ghent-2DPAGE; 1525; IEF.
Aarhus/Ghent-2DPAGE; 1526; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peroxisome; NADP; 3D-structure.
                                                                                                                                                                                                                                                                                     AL035079; CAB45236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59625 MW;
                                                                                                                                                                                                                                                                EMBL; X04076; CAA27717.1; -. EMBL; K02400; AAB59522.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00199; catalase; 1
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100W; 14-JUN-99.
1DGB; 11-FEB-00.
1DGF; 11-FEB-00.
1DGG; 17-FEB-00.
1DGH; 17-FEB-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A23646.
A23651.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A00501;
A23646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A23651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 115500;
                                                          PEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'NIT_MET
                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                             MBL;
                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                        MBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
PIR;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                  MEDLINE-95286491; PubMed-7768808;
Rocha E.R., Smith C.J.;
"Biochemical and genetic analyses of a catalase from the anaerobic
                                                                                                                                            Bacteroides fragilis.
Bacteria, CFB group, Bacteroidetes; Bacteroidales; Bacteroidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROXIMAL HEME LIGAND (BY SIMILARITY). 4F28A24ED9B9A966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: HOMODIMER.
-i- INDUCTION: UPREGULATED BY OXYGENATION AND STATIONARY PHASE.
-i- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.4%; Score 65; DB 1; Length 486; 55.2%; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000510; Catalase; 1. PROSITE; PS00437; CATALASE_1; 1. PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 E
55905 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18676; AAC43384.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00199; catalase; 1. PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 55.2 ses 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 3
486 AA;
                                                                                                                                                                                                               NCBI_TaxID=817;
                                                                                                                               KATA OR KATB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATA_HAEIN
P44390;
                                                                                                                                                                                             Bacteroides
CATA_BACFR
P45737;
                                                                                                                                                                                                                                                                                  STRAIN=638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
CATA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12415
```

Gaps

ö

42.0%; Score 66; DB 1; Length 526; 66.7%; Pred. No. 0.026; 1ive 0; Mismatches 7; Indels

```
9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
                                                                                                                                         CATA_CANFA
                                                                                                                                                                                        SOUTH THE TEXT TO 
                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Fittier of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERVES
                                                                                                                                                                                                                               Bishai W.R., Smith H.O., Barcak G.J.;
"A peroxide/dascorbate-inducible catalase from Haemophilus influenzae is homologous to the Escherichia coli katE gene product.";
J. Bacteriol. 176:2914-2921(1994).
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=RD KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
UtterDack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
--- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; STO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
--- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
                           Haemophilus influenzae.
Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}.\,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N -> C (IN REF. 1).
N -> T (IN REF. 1).
N -> S (IN REF. 1).
N -> T (IN REF. 1).
N -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: HEME GROUP.
-!- SUBGNIT: HOMOHEXAMER (BY SIMILARITY).
-!- SUBCILILAR LOCATION: CYTOPIASMIC (Probable).
-!- INDUCTION: BY HYDROGEN PEROXIDE.
-!- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                 STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-94245618; PubMed-8188593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0067; CATALASE.
PRODSITE; PRO00437; CATALASE.1; 1.
PROSITE; PS00437; CATALASE.2; 1.
PROSITE; PS00438; CATALASE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57680 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U02682; AAA20441.1; -. EMBL; U32774; AAC22587.1; -.
Catalase (EC 1.11.1.6)
KATA OR HKTE OR HI0928
                                                                                                                                                                                                                                                        "A peroxide/ascorbat
is homologous to the
J. Bacteriol. 176:29
[2]
SEQUENCE FROM N.A.
STRAIN=RD / KW20 / A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346
357
384
413
423
508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIGR; HI0928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                          "CDNA sequence and deduced amino acid sequence of dog catalase.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL BEROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROXIMAL HEME LIGAND (BY SIMILARITY). CB00F7F88FE2D972 CRC64;
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEROXIDE.
-:- CATALVIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
-:- SUBGUIT: HONDETRAMER (BY SIMILARITY).
-:- SUBCELLUIAR LOCATION: Peroxisomal (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.4%; Score 65; DB 1; 61.9%; Pred. No. 0.037;
                                           16-077-2001 (Rel. 40, Created)
16-077-2001 (Rel. 40, Last sequence update)
16-077-2001 (Rel. 40, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATA_CAVPO

ID CATA_CAVPO

TO CATA_CAVPO

O04405; 090251;
DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB012918; BAA36420.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                                                                                                                                                                                                                                                                                                           STRAIN-BEAGLE; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 TTGGGNPIGDKLNVMTAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00199; catalase; 1
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
  STANDARD;
                                                                                                                                                                                  Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
357
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peroxisome.
  CATA_CANFA
097492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INIT_MET
```

Gaps

ö

6; Indels

DB 1; Length 508;

41.4%; Score 65; DB 1; 61.9%; Pred. No. 0.035; iive 2; Mismatches

Conservative

Best Local Similarity Matches 13; Conserv

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                    Saruyama H., Matsumura T.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLE FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                  PEROXIDE.
-:- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-:- COFACTOR: HEME GROUP (BY SIMILARITY).
-:- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: PEROXISOMAL and glyoxysomal (By similarity).
-:- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                       Triticum aestivum (Wheat).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
Catalase (EC 1.11.1.6).
Helianthus annuus (Common sunflower).
Helianthus annuus (Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. SPANNERS ALLZWECK; TISSUE-Cotyledon;
MEDLINE-95101741; Pubmeds 7803505;
Kleff S., Trelease R.N., Eising R.;
"Nucleotide and deduced amino acid sequence of a putative higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 1; Length 492;
Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D86327; BAA13068.1; -.
HSSP; P00432; 4BLC.
IHCPPCO; IPR002226; Catalase.
Pfam; PF00199; catalase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 TTAFGAPVWDDNNVITAGPRG
    Catalase 1 (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heliantheae; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATA_HELAN
P45739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATA_HELAN
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                               STRAIN=HARTLEY; TISSUE=Lung;
MEDLINE=96180120; PubMed=8597602;
Yuan H.T., Bingle C.D., Kelly F.J.;
"Differential patterns of antioxidant enzyme mRNA expression in guinea pig lung and liver during development.";
Biochim. Biophys. Acta 1305:163-171(1996).
-!- FUNCTION: OCCURS IN ALMOST ALL ARROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROXIMAL HEME LIGAND (BY SIMILARITY). MISSING (IN REF. 2).
                                                        Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; P0000510; Caralase; 1.
PROSITE; PS00437; CATALASE_1; 1.
PROSITE; PS00438; CATALASE_2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP; Peroxisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                              Pinteric M., Baumgart E., Bulitta C., Fahimi D., Voelkl A.; "Molecular characterization of guinea pig catalase."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        PEROXIDE.
--- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
--- CONGTOR: HEBE GROUD AND NADP (BY SIMILARITY).
--- SUBGNAT: HOMOTETRAMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: PEROXISOMA1 (BY SIMILARITY).
--- THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> G (IN REF. 2).
7B58FDD76255E276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1;
Pred. No. 0.037;
16-OCT-2001 (Rel. 40, Last annotation update) Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ005111; CAB57222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro: IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 A
59802 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TTAGGNPVGDKLNIMTVGPRG 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.48; 61.98;
                                                                                                                                                                                                                                               [2]
SEQUENCE OF 1-137 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39841; AAC52717.1;
HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                     NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAT1_WHEAT
Q43206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
CAT1_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

ö

Gaps

ö

Indels

.. 2

q

ó

검검검장

SIMILARITY).

```
COFACTOR: HEME GROUP AND NADP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: August 22, 2002, 07:45:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Job time: 158 sec
                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
Ken C.F., Lin C.T., Wu J.L., Shaw J.F.;
"Molecular cloning of a cDNA coding for catalase from zebrafish (Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
-!- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
                                   SERVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Gerhard G.S., Kauffman E.J., Grundy M.A.;
"Molecular cloning and sequence analysis of the Danio rerio catalase gene.";
Comp. Biochem. Physiol. 127:447-457(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
molecular weight precursor for catalase in sunflower cotyledons.";
Blochim. Blophys. Acta 1224:463-466(1994).

Blochim. Blophys. Acta 1224:463-466(1994).

TO PROTECT CELCA HYDROGEN PEROXIDE IN WATER AND OXYGEN; SER TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.

-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

-!- CORACTOR: HEME GROUP.

-!- SUBGELLULAR LOCATION: Peroxisomal (By similarity).

-!- SUBCELLULAR LOCATION: PEROXISOMAL (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PROXIMAL HEME LIGAND (BY SIMILARITY).

4ASCS96S06F4496I CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii; Teleostei; Euteleostei: Ostariophysi;
Cypriniformes: Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 40.8%; Score 64; DB 1; Length 492; Il Similarity 57.1%; Pred. No. 0.048; 12; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATA_BRARE STANDARD; PRT; 526 AA. 09PT92; 0918V5; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                             InterPro; IPR002226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56755 MW;
                                                                                                                                                                                                                                                                 EMBL; L28740; AAA69866.1; -. HSSP; P00432; 4BLC.
                                                                                                                                                                                                                                                                                                                                                                                                                   65
138
348
392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Peroxisome.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 40
CATA_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                           HSSP; P00432; 4BLC.

SIN; ZDB-GENE-000210-20; cat.

InterPro; IPR002205; Catalase.

Pfam; PF00199; Catalase; 1.

PRINTS; PR00067; CATALASE.

PRODM; PD000510; Catalase; 1.

PROSITE; PS00438; CATALASE_1; 1.

PROSITE; PS00438; CATALASE_2; 1.

Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 1; Length 526; Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V -> A (IN REF. 2).
P -> S (IN REF. 2).
T -> I (IN REF. 2).
S -> F (IN REF. 2).
MIQ. -> NAA (IN REF. 2).
M -> T (IN REF. 2).
W -> T (IN REF. 2).
W -> T (IN REF. 2).
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Peroxisomal (By similarity).
SIMILARITY: BELONGS TO THE CATALASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ?
                                                                                                                                                                                                                                                                       EMBL; AJ007505; CAB64949.1; -. EMBL; AF170069; AAF89686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
59654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
148
358
110
123
152
161
352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peroxisome; NADP.
```

		0
		•

Title: Perfect score:

Sequence:

OM protein -

ü

Scoring table:

Searched:

Database

```
AAG43132
AAG43132
AAG43132
AAG43132
AAG43132
AAG219059
AAG219059
AAG219059
AAG219059
AAG219059
AAM40233
AAM40233
AAM4023117
AAM40348
AAM40348
AAM40348
AAM40348
AAM40348
AAM40348
AAM40348
AAM40348
AAM40436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB93827
AAY23609
AAU44929
AAW99183
AAY97052
AAU38392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62880
AAG32317
AAG45498
AAG32316
47.5
47.5
47
47
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.5
46.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal sequence
Helicobacter CP2 a
Helicobacter CP2-P
Helicobacter CP2-P
H. pylori GHPO 358
Helicobacter pylor
Helicobacter pylor
Arabidopsis thalia
Arabidopsis thalia
Clone of A. thalia
                                                                                                                                                                                                                            A_Geneseq_012802;*

| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983_DAT:*
| SIDS1/gcgdata/hold-geneseq-embl/AA1985_DAT:*
| SIDS1/gcgdata/hold-geneseq-embl/AA1986_DAT:*
| SIDS1/gcgdata/hold-geneseq-embl/AA1980_DAT:*
| SIDS1/gcgdata/hold-geneseq-embl/AA1980_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980_DAT:*
| SIDS1/gcgdata/hold-geneseqy-embl/AA1990_DAT:*
                                                   August 22, 2002, 07:44:04; Search time 51.87 Seconds (without alignments) 62.100 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.pylori catalase
                                                                                                                                                                                                                                                                                                                                                                                                                         he number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                    1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                           747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW33405
AAW06481
AAW06482
AAW98423
AAW54146
AAW52810
AAG23826
AAG23826
AAY18131
                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR88244
                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                US-09-488-737-2
157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score greater thar and is derived by
                                                                                                                                                                                                                                                                                                                                                                                                                           is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0
100.0
100.0
100.0
100.0
100.0
97.5
47.8
```

Tobacco salicylic Amino acid sequenc Human tyrosine dep Propionibacterium Human 155 lipoxyge Human 155 lipoxyge Murine Wnt-8D prot Human Wnt3 (ZWht3) C glutamicum prote

C glutemicum protection of glutemicum protection of glutemicum SRT Drosophila melanog SepB protein encod Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Novel human diagno proteinase K varia E. coli cellular p Novel human diagno Novel human diagno of cellular p

Pred. No.

Score

Result No.

157 157 157 157 157 157 153 75 75

Rhodococcus sp. oh Salmonella typhi c Amino acid sequenc Arabidopsis thalia Arabidopsis thalia

Human secreted pro Human protein sequ Canine hookworm ne Propionibacterium Rhodococcus corall

Propionibacterium

Arabidopsis thalia Arabidopsis thalia Bacillus thermoglu Zea mays procein f Arabidopsis thalia H. pylori 63 kD ad Peptide #309 enco Peptide #309 enco Peptide #3012 enco Peptide #305 enco Peptide #305 enco Peptide #306 enco Peptide #3154 enco Bacillus thermoglu V. rumoiensis S-1 Recombinant catala Catalase Seq Human protein SEQ Human protein SEQ Human protein SEQ Mheat catalase pro Rat mitogenic regul Rat mitogenic regul Rat mitogenic regul Human mitogenic regulatial sequence O Statalase-R. Asper Aspergillus niger Catalase-R. Aspergillus niger Colvel human diagno

AAW33405 standard; peptide; 29 AA.

AAW33405

RESULT

AAW33405;

```
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human protein SEQ
Human polypeptide
                                                                Arabidopsis thalia
Arabidopsis thalia
                                                                                                     Drosophila melanog
Candida albicans,
                                                                                                                      Human pancreatic G
                                                                                                                                         Human protein sequ
                                                                                                                                 Glycosyl-phosphati
                                                                                  Human protein SEQ
                                                                                            Human polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The N-terminal sequence of the 54 kD monomeric subunit of the Helicobacter pylori ATCC 43579 catalase. The complete catalase (a tetrameric protein) can be used in compsns. for immunising against H.pylori, pref. those implicated in gastritis, peptic ulcers and stomach cancer. The compsns. contain inactive mutant forms of the catalase and may also contain adjuvants e.g. alum, and other H.pylori antigens e.g. urease. The compsns. are pref. encapsulated in liposomes.
                                                                                                                                                                                                                                                                                    Helicobacter pylori; catalase; immunisation; gastritis; peptic ulcer; stomach cancer; mutant; antigen; urease; encapsulate; liposome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccines against Helicobacter pylori – contg. H. pylori catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 157; DB 16;
100.0%; Pred. No. 6.8e-17;
ive 0; Mismatches 0;
                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                      (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
                                             AAM78945
AAM39546
                                                                                                                              AAR75111
AAB92908
                                                              AAG52458
          AAG52460
                            AAG52459
                                                                         AAG45660
                                                                                 AAM79929
                                                                                            AAM41332
                                                                                                    ABB57901
 AAB93714
                                    AAG45661
                                                                                                                      AAR22277
                                                                                                                                                                                                            AAR88244 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 4; 14pp; French.
                                                                                                                                                                                                                                                                  H.pylori catalase N-terminus.
 95WO-FR00383
                                                                                                                                                                                                                                                                                                                                                                                    94FR-0004172
                                                                                                                                                                                                                                                 (first entry)
 445
672
680
721
721
751
775
802
                                                                                         802
187
189
316
316
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-366230/47.
                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
29.0
29.0
29.0
29.0
29.0
29.0
29.0
28.7
28.7
28.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 AA;
                                                                                                                                                                                                                                               17-MAY-1996
                                                                                                                                                                                                                                                                                                                               W09527506-A1
                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 29;
                                                                                                                                                                                                                                                                                                                                                19-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                        Lissolo L;
AAR88244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                   AAR88244
RESULT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New purified Helicobacter pylori proteins are obtained from a membrane fraction and have apparent molecular weights (by electrophoresis on = 10% polyacrylamide gel in presence of SDS) of 54, 50, 32-35 and 30 kD respectively, of which the 54 kD protein does not react with anti-catalase antiserum. The present sequence represents the N-terminal of the 54 kD protein. The proteins and purified peptides derived from them can be used (by active immunisation) to treat or prevent H. pylori infections (gastritis, peptic ulcers, gastric cancer etc.). Antibodies raised against the protein can be used for psssive immunisation. Derived peptides and antibodies are also useful as reagents for diagnostic immunoassays, and antibodies are further useful for affinity purification of the new proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 29;
                                                                                                                                                                                                                                                                                                                                                                                              New Helicobacter pylori membrane proteins - and related polypeptide(s) and antibodies, useful for active or passive immunisation and diagnosis
                                                                                                          diagnostic; affinity purification; gastritis; peptic ulcer; gastric cancer.
                                                                      N-terminal sequence of 54 kD membrane protein of H. pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                    vaccine; immunisation; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 157; DB 18;
100.0%; Pred. No. 6.8e-17;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CP2; antigen; vaccine; diagnosis; gastritis.
                                                                                                                                                                                                                                                                                                            (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 25; 48pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505
                                                                                                                                                                                                                                                    96WO-FR01552,
                                                                                                                                                                                                                                                                               95FR-0011890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW06481 standard; Protein;
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CP2 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                             Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-226163/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                      membrane protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 AA;
                                                                                                                                                                                          WO9712909-A1
                                                                                                                                                                                                                                                  04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
                                                                                                                                                                                                                                                                               04-OCT-1995;
                                         05-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1997
                                                                                                                                                                                                                       10-APR-1997
                                                                                                                                                                                                                                                                                                                                        Lissolo L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW06481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

Gaps

ö

Indels

MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29

g ô

Conservative

 \sim

;

Gaps

;

Indels

ö

Mismatches

;

Conservative

29;

Matches

```
Helicobacter pylori ATCC 43504 CP2 antigen (AAW06481) is useful in the specific and quantitative detection of H. pylori and in vaccine prodn. CP2 antibody titre shows high correlation with the pathology of gastritis. The CP2 amino acid sequence was deduced from a genomic clone (AAT45042). Slightly different sequences, CP2-PCR1 (AAW06482) and CP2-PCR2 (AAW06483), were deduced from clones (AAT45042-43) obtd. by PCR amplification. Isolation of the gene sequences allows the mass prodn. of recombinant CP2 in transformed host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residue 449 is Gly in CP2-PCR1 and CP2-PCR2 and
                                                                 'note= "residue 130 is Asp in CP2-PCR2"
                                                                                           'note= "residue 160 is Pro in CP2-PCR2"
                                                                                                                      note= "residue 218 is Leu in CP2-PCR2"
                                                                                                                                               note= "residue 234 is Ile in CP2-PCR2"
                                                                                                                                                                                                     note= "residue 248 is Asp in CP2-PCR2"
                                                                                                                                                                                                                                'note= "residue 262 is Ile in CP2-PCR2"
                                                                                                                                                                                                                                                         note= "residue 285 is Cys in CP2-PCR2"
                                                                                                                                                                                                                                                                                    'note= "residue 287 is Lys in CP2-PCR2"
                                                                                                                                                                                                                                                                                                             'note= "residue 292 is Thr in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                        note= "residue 316 is Thr in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                   'note= "residue 344 is Cys in CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                              'note= "residue 358 is Arg in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "residue 397 is Thr in CP2-PCR2"
                                                                                                                                                                         'note= "residue 237 is His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama T,
            Helicobacter pylori strain ATCC 43504
                               Location/Qualifiers
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 16-18; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WAKP ) WAKO PURE CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0083512.
95JP-0136564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96EP-0108637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawabata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-013697/02.
N-PSDB; AAT45041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 AA;
                                                 Misc-difference
                                                                            Misc-difference
                                                                                                       Misc-difference
                                                                                                                                  Misc-difference
                                                                                                                                                            Misc-difference
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hirayasu K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP745674-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
```

Score 157; DB 18; Pred. No. 1.7e-15;

100.0%; 100.0%;

Query Match Best Local Similarity

```
Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "residue 397 is Thr in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "residue 130 is Asp in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "residue 160 is Pro in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "residue 234 is Ile in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "residue 262 is Ile in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CP2-PCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CP2-PCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in CP2-PCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is Leu in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "residue 237 is His in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "residue 248 is Asp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is Cys in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanaka
                                                                                                                                                                                                                                                                                                                                                antigen; vaccine; diagnosis; gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "residue 287 is Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "residue 316 is Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue 344 is Arg
and CP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "residue 449 is Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugiyama T,
1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori strain ATCC 43504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "residue 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "residue 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "residue 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "residue 358
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                        AAW06482 standard; Protein; 505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (WAKP ) WAKO PURE CHEM IND LTD
                                                                                                                                                                                                                                                                                                       Helicobacter CP2-PCR1 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0083512.
95JP-0136564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96EP-0108637
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawabata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-013697/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT45042
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirayasu K,
                                                                                                                                                                                                                                                       24-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP745674-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-DEC-1996
                                                                                                                                                                                                           AAW06482;
                                                                                                                                       AAW06482
                                                                                                                 RESULT
                                                                                                                                                                                                           A CONTRACTOR OF A CONTRACTOR O
  ò
                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 505
                                                                                                                                                                                                                                                       in CP2-PCR2"
```

Tanaka T;

```
WPI; 1997-013697/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori
                                                                                                                                                                                                                                                                                                                505 AA;
                                                                                                                                N-PSDB; AAT45043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Al-Garawi A,
                               30-MAY-1996;
                                                                                                    Hirayasu K,
                                                   05-APR-1996;
                                                            02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-1997;
            04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW98423;
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW98423
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                          ö
                                    in the specific and quantitative detection of H. pylori and in vaccine prodn. CP2 antibody titre shows high correlation with the pathology of gastritis. The CP2-PCR1 amino acid sequence was deduced from a DNA clone (AAT45642) obtd. by PCR amplification. Slightly different sequences were deduced for CP2 (AAW06481) from genomic DNA (AAT45041) and for CP2-PCR2 (AAW06483) from a PCR fragment (AAT45043) derived from a clinical isolate. Isolation of the gene sequences allows the mass prodn. of recombinant CP2 in transformed
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue 130 is Asn in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "residue 160 is His in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "residue 234 is Val in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "residue 248 is Asn in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in CP2 and CP2-PCR1"
                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "residue 285 is Tyr in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "residue 287 is Gln in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in CP2 and CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "residue 397 is Ala in CP2 and CP2-PCR1"
                             ATCC 43504 CP2-PCR1 antigen (AAW06482) is
                                                                                                                                                                     Length 505;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in CP2-PCR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue 449 is Arg in CP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               in CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in CP2
                                                                                                                                                                    100.0%; Score 157; DB 18;
100.0%; Pred. No. 1.7e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            CP2; antigen; vaccine; diagnosis; gastritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residue 218 is His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "residue 237 is Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "residue 262 is Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "residue 316 is Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "residue 344 is Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residue 292 is Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "residue 358 is Lys
                                                                                                                                                                                                            1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                     Claim 1; Page 18-20; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                               AAW06483 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                        CP2-PCR2 antigen
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                             Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 130
                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 234
                                                                                                                                         505 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                        Helicobacter
                                                                                                                                                                                                                                                                                                                     24-FEB-1997
                                                                                                                    host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP745674-A2
                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                   AAW06483;
                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                     AAW06483
                                                                                                                                                                                                                                                            RESULT
ò
                                                                                                                                                                                                                             a
```

```
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                          Helicobacter pylori CP2 antigen structural polypeptide(s) - also corresponding DNA, useful as reagents for detecting H. pylori and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori CP2-PCR2 antigen (AAW06483) is useful in the specific and quantitative detection of H. pylori and in vaccine prodn. CP2 antibody titre shows high correlation with the pathology of gastritis. The CP2-PCR2 amino acid sequence was deduced from a DNA clone (AAT45043) obtd. by PCR amplification of DNA from H. pylori isolated from a patient with chronic gastritis. Slightly different sequences were deduced for CP2 (AAW06481-82) from H. pylori ATCC 43504. Isolation of these gene allows the mass prodn. of recombinant CP2 in transformed host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomb J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 157; DB 18;
100.0%; Pred. No. 1.7e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                             Tanaka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kleanthous H, Miller C,
                                                                                                                                                                                             Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 21-23; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW98423 standard; Protein; 505 AA
                                                                                                                                     (WAKP ) WAKO PURE CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0902615.
97US-0833457.
97US-0881227.
                                                 96JP-0083512.
95JP-0136564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCI INC
96EP-0108637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US06371.
                                                                                                                                                                                                                                                                                                                                                                                       the production of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori GHPO 358 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                             Kawabata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENOME
```

Gaps

```
The Helicobacter pylori catalase is a protein of 58650 Da. The protein, gene sequence and products, such as an immunogenic fragment, can be used for the treatment or prevention of Helicobacter infection, particularly H. pylori infections which cause gastroduodenal disease. They can also be used for the detection and diagnosis of Helicobacter infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease
                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                 Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 505;
                                                                                                                                                                                                                                                                                Treatment; prevention; gastroduodenal disease; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
              Score 157; DB 19;
Pred. No. 1.7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 153; DB 19;
Pred. No. 7.1e-15;
 100.0%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Radcliff FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                      Helicobacter pylori isolate RU1 catalase
                                                                     1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                     Disclosure; Page 33-34; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG23827 standard; Protein; 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CSLC-) CSL LTD.
(UYNE-) UNIV NEW SOUTH WALES
                                                                                                                                                                    AAW52810 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                            97WO-AU00515
                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0695987
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.5
Best Local Similarity 96.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doidge CV, Hazell SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-159544/14.
                                                                                                                                                                                                                                                                                                           Helicobacter pylori
                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV20910
                                                                                                                                                                                                                                                                                                                                      WO9806853-A1
                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1996;
                                                                                                                                                                                                                         20-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG23827;
                 Query Match
                                                                                                                                                                                               AAW52810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                          Matches
                                                                                                                                                     AAW52810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG23827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                              g
                                                                                                                                                                                  DX LX K
                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                  ğ
                                                                                                                       This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Helicobacter pylori catalase is a protein of 58650 Da. The protein, gene sequence and products, such as an immunogenic fragment, can be used for the treatment or prevention of Helicobacter infection, particularly H. pylori infections which cause gastroduodenal disease. They can also be used for the detection and diagnosis of Helicobacter infection.
                                     New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Helicobacter catalase nucleic acid - used to develop products for the treatment or prevention of Helicobacter infection, particularly H. pylori gastroduodenal disease
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                             Length 505;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ireatment; prevention; gastroduodenal disease; detection.
                                                                                                                                                                                                                                                                            ch 100.0%; Score 157; DB 19; Similarity 100.0%; Pred. No. 1.7e-15; 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori isolate 921023 catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radcliff FJ;
                                                                                            Claim 8; Page 711-713; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 37-38; 46pp; English
                                                                                                                                                                                                                                                                                                                                     1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW54146 standard; Protein; 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CSLC-) CSL LTD.
(UYNE-) UNIV NEW SOUTH WALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-AU00515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0695987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-1998 (first entry)
                                                                                                                                                                                                         detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doidge CV, Hazell SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-159544/14.
WPI; 1998-542293/46.
N-PSDB; AAX14142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                     505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV20911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9806853-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1998,
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW54146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                        Matches
 ò
                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

Arabidopsis thaliana protein fragment SEQ ID NO: 27277.

```
9905 - 0140354
9905 - 0140354
9905 - 0140823
9905 - 0140823
9905 - 0142184
9905 - 0142184
9905 - 0142184
9905 - 0142180
9905 - 0142390
9905 - 0142390
9905 - 0144332
9905 - 0144332
9905 - 0144333
9905 - 0144333
9905 - 0144333
9905 - 0144333
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0144335
9905 - 0145086
9905 - 0145086
9905 - 0145086
9905 - 0145086
9905 - 014536
9905 - 014536
9905 - 014536
9905 - 014536
9905 - 014536
9905 - 014536
9905 - 014538
9905 - 014538
9905 - 014538
9905 - 014538
9905 - 014538
9905 - 014538
9905 - 014538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990S-0147192.
990S-0147260.
990S-0147303.
990S-0147416.
990S-0147933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0148319.
990S-0148365.
990S-0148565.
990S-0148684.
990S-0149368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0149722.
990S-0149723.
990S-0149929.
990S-0149902.
990S-0149930.
990S-0150884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0151066.
99US-0151080.
99US-0151303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0151065
 23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
20 - JUL - 1999;
                                                                                                                                                                                                                                                                                                     21-JUL-1999;
21-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                     22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           28 - JUL - 1999

02 - AUG - 1999

02 - AUG - 1999

03 - AUG - 1999

04 - AUG - 1999

05 - AUG - 1999

06 - AUG - 1999

06 - AUG - 1999

07 - AUG - 1999

11 - AUG - 1999

12 - AUG - 1999

13 - AUG - 1999

13 - AUG - 1999

14 - AUG - 1999

17 - AUG - 1999

18 - AUG - 1999

18 - AUG - 1999

18 - AUG - 1999

20 - AUG - 1999

20 - AUG - 1999

21 - AUG - 1999

22 - AUG - 1999

23 - AUG - 1999

24 - AUG - 1999

25 - AUG - 1999

26 - AUG - 1999

27 - AUG - 1999

28 - AUG - 1999

28 - AUG - 1999

29 - AUG - 1999

20 - AUG - 1999

21 - AUG - 1999

22 - AUG - 1999

23 - AUG - 1999

24 - AUG - 1999

25 - AUG - 1999

26 - AUG - 1999

27 - AUG - 1999

28 - AUG - 1999

28 - AUG - 1999

29 - AUG - 1999

20 - AUG - 1999

21 - AUG - 1999

22 - AUG - 1999

23 - AUG - 1999

24 - AUG - 1999

25 - AUG - 1999

26 - AUG - 1999

27 - AUG - 1999

28 - AUG - 1999

28 - AUG - 1999

29 - AUG - 1999

20 - AUG - 1999

20 - AUG - 1999

21 - AUG - 1999

22 - AUG - 1999

24 - AUG - 1999

25 - AUG - 1999
                                                                                                                                                                                                                                                                                                                                                                                        -JUL-1999;
-JUL-1999;
-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1999
   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                     990S - 0.121825

990S - 0.123180

990S - 0.123788

990S - 0.125788

990S - 0.125788

990S - 0.125785

990S - 0.128714

990S - 0.128714

990S - 0.131449

990S - 0.131484

990S - 0.131488

990S - 0.131458

990S - 0.131458
                                                                                                                   2000EP-0301439
                                                  Arabidopsis thaliana
                                                                                                                                    25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
11-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
                                                                                                                 25-FEB-2000;
                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -MAY-1999;
-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-19
01-JUN-19
03-JUN-19
04-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -JUN-19
-JUN-19
-JUN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JUN-
```

€

```
9905-0135629
9905-0136621
9905-0136782
9905-0137528
9905-0137528
9905-0137504
9905-013754
9905-0138847
9905-0138847
9905-0139453
9905-0139455
9905-0139456
9905-0139456
9905-0139456
9905-0139461
9905-0139461
9905-0139461
9905-0139461
9905-0139461
9905-0139461
9905-0139463
                                                                                                                           990S - 0128714.
990S - 0128714.
990S - 0130477.
99US - 0130449.
99US - 0130891.
99US - 013248.
99US - 0132484.
99US - 0132486.
99US - 0132486.
99US - 0132486.
                                                    99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                       99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
                                                                                                                                                                                                                                                                                          99US-0134768.
99US-0134768.
99US-0134941.
                                                                                                                                                                                                                                                                  99US-0134218
                                                                                                                                                                                                                                                                         99US-0134219.
                                                                                                                                                                                                                                                                                                                    99US-0135124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0141842
                                    2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0140991
99US-0141287
                                                             05-MAR-1999)
09-MAR-1999)
09-MAR-1999)
01-APR-1999)
01-APR-1999)
01-APR-1999)
01-APR-1999)
02-APR-1999)
03-APR-1999)
04-MAY-1999)
05-MAY-1999)
06-MAY-1999)
06-MAY-1999)
06-MAY-1999)
06-MAY-1999)
07-JUN-1999)
08-JUN-1999)
08-JUN-1999)
09-JUN-1999)
 EP1033405-A2
                                   25-FEB-2000;
  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 21; Length 377; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 27276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG23826 standard; Protein; 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || || || || || || || || || || || tinsgapvwnnnssmtvgprg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                               990S-0158369.
990S-0159294.
990S-0159294.
990S-0159329.
990S-0159339.
                                                                                                                                                                                                                                                                                                                                                       990S-0161406.
990S-0161359.
990S-0161360.
990S-0161361.
990S-0151438.
990S-0151930.
990S-0151930.
990S-0153078.
990S-0154039.
990S-0154039.
990S-0155486.
990S-0155486.
990S-0155659.
990S-0155659.
990S-0157137.
                                                                                                                                                                                                                             99US-0159637.
99US-0159638.
99US-0159584.
99US-0160741.
                                                                                                                                                                                                                                                                                                                                                                                                    99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%;
                                                                                                                                                                                                                                                                99US-0160767.
99US-0160768.
99US-0160770.
                                                                                                                                                                                                                                                                                          99US-0160814.
99US-0160815.
99US-0160980.
                                                                                                                                                                                                                                                                                                                    99US-0160981
                                                                                                                                                                                                                                                                                                                                      99US-0161404
99US-0161405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.99
watches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
31-AuG-1999;
01-SEP-1999;
10-SEP-1999;
13-SEP-1999;
13-SEP-1999;
20-SEP-1999;
22-SEP-1999;
24-SEP-1999;
24-SEP-1999;
25-SEP-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
15-OCT-1999;
16-OCT-1999;
17-OCT-1999;
16-OCT-1999;
17-OCT-1999;
18-OCT-1999;
18-OCT-1999;
18-OCT-1999;
18-OCT-1999;
18-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
27-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG23826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
```

9 0 œ

```
990S-0142154.
990S-0142390.
990S-0142390.
990S-0142300.
990S-0142977.
990S-0143542.
990S-0144085.
990S-0144332.
990S-0144333.
990S-0144334.
990S-0144335.
                                                                                                                                                               990S - 0144814
990S - 0145086
990S - 0145085
990S - 0145089
990S - 0145192
990S - 0145192
990S - 0145145
990S - 0145218
990S - 0145218
990S - 0145218
990S - 0145913
990S - 0145913
990S - 0145913
990S - 0145913
990S - 0147192
990S - 0147192
990S - 0147192
990S - 0147193
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0149723.
99US-0149723.
99US-0149929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0149930.
99US-0150566.
99US-0150884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0151065.
99US-0151066.
99US-0151080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0153070.
99US-0153758.
99US-0154018.
99US-0154039.
01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
06-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
16-JUL-1999;
16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
                                                                                                         19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 - AUG - 1999;
23 - AUG - 1999;
26 - AUG - 1999;
27 - AUG - 1999;
30 - AUG - 1999;
31 - AUG - 1999;
31 - AUG - 1999;
01 - SEP - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
                                                                                                                                                                                                                  :666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1999
                                                                                                                                                                                                                                                                                                                03-AUG-19
04-AUG-19
04-AUG-19
                                                                                                                                                                                                                                                                                                                                        05-AUG-19
05-AUG-19
06-AUG-19
                                                                                                                                                                                                                                                                                                                                                                       09-AUG-19
09-AUG-19
10-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-19
12-AUG-19
13-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1
                                                                                                                                                                                                                                                                                                                                                                06-AUG-1
```

```
Strong light adapting condition; light-resistant plant; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.8%; Score 75; DB 21; Length 394; 61.9%; Pred. No. 0.0042; 1ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone of A. thaliana strong light adapting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18131 standard; Protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
990S-0154779-
990S-0155866-
990S-0155659-
990S-0155659-
990S-0156596-
990S-0157117-
990S-0157865-
990S-0157865-
990S-0157865-
990S-0158029-
990S-0159294-
990S-0159294-
990S-0159294-
990S-015930-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0160814.
990S-0160815.
990S-0160980.
990S-0160981.
990S-0160989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0161406.
99US-0161359.
99US-0161360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SUMO ) SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 61.9%;
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97JP-0306044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0306044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
                  22 - SEP - 1999;
24 - SEP - 1999;
24 - SEP - 1999;
26 - SEP - 1999;
26 - CCT - 1999;
27 - CCT - 1999;
28 - CCT - 1999;
29 - CCT - 1999;
213 - CCT - 1999;
213 - CCT - 1999;
214 - CCT - 1999;
214 - CCT - 1999;
214 - CCT - 1999;
215 - CCT - 1999;
216 - CCT - 1999;
217 - CCT - 1999;
217 - CCT - 1999;
218 - CCT - 1999;
218 - CCT - 1999;
219 - CCT - 1999;
21
                                                                                                                                                                                                                                                                                                                                                         14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP11137253-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY18131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
990S - 0.139454 - 990S - 0.139455 - 990S - 0.139456 - 990S - 0.139459 - 990S - 0.139461 - 990S - 0.139462 - 990S - 0.139750 - 990S - 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             990S-0138094
990S-0138847
990S-0138147
990S-0139452
990S-0139453
                                                                                                                           990S-0132484.
990S-0132485.
990S-0132486.
990S-0132486.
                                                                                                                                                                                                             990S-0132863
990S-0134256.
990S-0134218.
990S-0134219.
                                                                                                                                                                                                                                                                                                                                                                99US-0134941.
99US-0135124.
99US-0135353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0140353.
99US-0140354.
99US-0140695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0142154.
99US-0142055.
99US-0142390.
                                                                                                                                                                                                                                                                                                                        99US-0134370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0136392
99US-0136782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0137222
99US-0137528
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0136021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0142803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0142920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0142977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0143624
99US-0144005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0144085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0144325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0144334
99US-0144335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0144331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0144333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99us-01
                   23 - APR - 1999;
28 - APR - 1999;
30 - APR - 1999;
30 - APR - 1999;
30 - APR - 1999;
65 - MAY - 1999;
66 - MAY - 1999;
77 - MAY - 1999;
11 - MAY - 1999;
11 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 - JUN - 1999

21 - JUN - 1999

22 - JUN - 1999

23 - JUN - 1999

24 - JUN - 1999

25 - JUN - 1999

26 - JUN - 1999

27 - JUN - 1999

28 - JUN - 1999

29 - JUN - 1999

20 - JUL - 1999

20 - JUL - 1999

20 - JUL - 1999

21 - JUL - 1999

22 - JUL - 1999

23 - JUL - 1999

24 - JUL - 1999

25 - JUL - 1999

26 - JUL - 1999

27 - JUL - 1999

28 - JUL - 1999

29 - JUL - 1999

20 - JUL - 1999

21 - JUL - 1999

21 - JUL - 1999

22 - JUL - 1999

23 - JUL - 1999

24 - JUL - 1999

25 - JUL - 1999

26 - JUL - 1999

27 - JUL - 1999

28 - JUL - 1999

28 - JUL - 1999

29 - JUL - 1999

20 - JUL - 1999

20 - JUL - 1999

21 - JUL - 1999

22 - JUL - 1999

23 - JUL - 1999

24 - JUL - 1999

25 - JUL - 1999

26 - JUL - 1999

27 - JUL - 1999

28 - JUL - 1999

29 - JUL - 1999

20 - JUL - 1999

20 - JUL - 1999

20 - JUL - 1999

21 - J
                                                                                                                                                                                                                                                                                                    16-JUL-1999;
16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-19
28-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1
24-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1
                                                                                                                                                                                                                                                                                                                          -MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L7 - JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1
    This sequence represents a clone of the protein of the invention.

The invention relates to a gene that is induced and expressed in a plant under a strong light adapting conditions, and is prepared by a procedure of the following light irradiations (1) to (3) is made on a plant already irradiated by a light irradiations (1) to (3) is made on a consisting of a continuous wave length component of a wave length region of 300-900 nm at 15 to 38 degrees C and the gene expression of which is induced in the cell of said plant: (1) A light of a light component of a wave length region of 300-700 mu E/sq. m s consisting of a continuous wave length component of a wave length region of 350-500 nm at 15-38 degrees C for 1 hour to several days; (2) a light of a light intensity of 200-600 mu E/sq. m s consisting of a continuous wave length component of a wave length region of 350-500 nm at 15-38 degrees C for several hours to several days; (3) a light of intensity 75-270 nm E/sq. m s consisting of a continuous wave length region of 300-800 nm continuous wave length component of a wave length region of 300-800 nm at 0-10 degrees C for several hours to several days. The method can be continuous wave length component of a wave length region of 300-800 nm continuous wave length region plant that is able to grow in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                 Induction of gene to be expressed in plant under a strong light adapting condition – useful for enabling plant to grow in desert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.8%; Score 75; DB 20; Length 492; 61.9%; Pred. No. 0.0054; Live 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 53875.
                                                                                                                                               Claim 7; Page 12-13; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG43132 standard; Protein; 492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9905-0123180
9905-0123180
9905-0125788
9905-0126264
9905-0126785
9905-0128714
9905-0128714
9905-0128945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.89
Best Local Similarity 61.99
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                 WPI; 1999-364702/31.
N-PSDB; AAX77100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG43132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG43132
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
990S-0144352.
990S-0144884.
990S-0144884.
990S-0145086.
990S-0145088.
990S-0145087.
990S-0145087.
990S-0145192.
990S-0145192.
990S-0145192.
990S-0145193.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145218.
990S-0145218.
                                                                                                                                                                                                                                                    990S-0146389.
990S-0147038.
990S-0147204.
990S-0147302.
990S-0147192.
                                                                                                                                                                                                                                                                                                                                           990S - 0147416
990S - 0147418
990S - 0148131
990S - 0148131
990S - 0148319
990S - 0148319
990S - 0149368
990S - 0149172
990S - 014972
990S - 014936
990S - 014936
990S - 014936
990S - 015106
990S - 015106
990S - 015106
990S - 015106
990S - 0151303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           990S-0156596.
990S-0157117.
990S-0157753.
990S-0157865.
990S-0158029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9905-0159293
9905-0159293
9905-0159294.
9905-0159295.
9905-0159329.
20 - JUL - 1999;
20 - JUL - 1999;
20 - JUL - 1999;
21 - JUL - 1999;
21 - JUL - 1999;
22 - JUL - 1999;
22 - JUL - 1999;
22 - JUL - 1999;
23 - JUL - 1999;
                                                                                                                                                                                                                              02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                          09-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                                                                                                         04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1999;
08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-15
16-AUG-15
17-AUG-19
18-AUG-19
20-AUG-19
20-AUG-19
23-AUG-19
23-AUG-19
                                                                                                                                                                                                                                                                   03-AUG-19
04-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SEP-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEP-1
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                       ö
                                                                                                                                                                                                      Score 75; DB 21; Length 492;
Pred. No. 0.0054;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 54930.
                                                                                                                                                                                                                                                                                                AAG43903 standard; Protein; 512 AA
                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                 || ||||||::|: :| ||||
ttnsgapvwnnnssmtvgprg 38
9905 - 0159331
9905 - 0159331
9905 - 0159638
9905 - 0159584
9905 - 0160767
9905 - 0160767
9905 - 0160814
9905 - 0160814
9905 - 0160816
9905 - 0160989
9905 - 0160980
9905 - 0161360
9905 - 0161360
9905 - 0161360
9905 - 0161360
9905 - 0161360
9905 - 0161360
                                                                                                                                                                                                      47.8%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0121825.
990S-0123180.
990S-0123788.
990S-0125788.
990S-0126264.
990S-0127465.
990S-0127465.
990S-012834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130077.
99US-0130449.
99US-0130510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0131449.
99US-0132048.
99US-0132407.
99US-0132484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0130891
                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                                                                      13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                              Local Similarity
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                                                                                    26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
119-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                  EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-1999
                                                                                                                                                                                                                                                                                                                AAG43903;
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                 RESULT 1
                                                                                                                                                                                                               Best
 Óγ
                                                                                                                                                                                                                                                    qq
```

```
PR 06-MW 1999; 9918-0132486
PR 10-MW 1999; 9918-0132486
PR 11-MW 1999; 9918-0132486
PR 11-MW 1999; 9918-0132486
PR 11-MW 1999; 9918-0132428
PR 12-MW 1999; 9918-0133421
PR 12-MW 1999; 9918-0133421
PR 22-MW 1999; 9918-0133421
PR 23-MW 1999; 9918-0133421
PR 24-MW 1999; 9918-0133421
PR 24-MW 1999; 9918-0133421
PR 28-MW 1999; 9918-0133421
PR 10-TUN-1999; 9918-0133422
PR 10-TUN-1999; 9918-0133422
PR 10-TUN-1999; 9918-0133422
PR 11-TUN-1999; 9918-0133422
PR 11-TUN-1999; 9918-0133422
PR 11-TUN-1999; 9918-0133452
PR 11-TUN-1999; 9918-013332
PR 11-T
```

90S-0145089 90S-0145089 90S-0145182 90S-0145218 90S-0145218 90S-0145218 90S-0145918 90S-0145918 90S-0145918 90S-0145918	905-014/038 905-014/038 905-014/302 905-014/303 905-014/303 905-014/416 905-014/416 905-014/8319 905-014/8319 905-014/8319 905-014/8319 905-014/8319 905-014/8319 905-014/9368 905-014/9368 905-014/9369 905-014/9309 905-014/9929 905-014/9929 905-014/9929	000000000000000000000 000 000000
22-JUL-1999 22-JUL-1999 8 23-JUL-1999 8 23-JUL-1999 8 23-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 27-JUL-1999 8 28-JUL-1999 8 28-JUL-1999	04 - Add - 1999 04 - Add - 1999 06 - Add - 1999 06 - Add - 1999 06 - Add - 1999 09 - Add - 1999 11 - Add - 1999 13 - Add - 1999 17 - Add - 1999 20 - Add - 1999 21 - Add - 1999 22 - Add - 1999 25 - Add - 1999 27 - Add - 1999 27 - Add - 1999	307-AU 30

```
Zea mays subsp. mays.
                                              Best Local Similarity
         483 AA;
                                                                                                                                                                                                                                                                                                                  25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                             23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
                                                                                                                                                                                                                                                                             EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-1999;
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1999;
21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                    25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1999
         Seguence
                                    Query Match
                                                                                                                                                             AAG19059;
                                                                                                                        12
                                                      Matches
                                                                                                                                  AAG19059
                                                                                                                        RESULT
 X S
                                                                          δλ
                                                                                            셤
                                                                                                                                           3
                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a catalase isolated from Bacillus thermoglucosidasius. A composition containing a B. thermoglucosidasius catalase is used to decompose hydrogen peroxide present in residual disinfectant remaining on a contact lens to avoid undesired injury to users. The catalase enzyme can also be used to treat textile substances which have been bleached with hydrogen peroxide. The catalase is derived from a non-mammalian source and reducing the need to use bovine liver catalases so the risk of cross infection from cows to humans is reduced. The production procedure is simple and has low cost with high yield of enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated catalase gene derived from Bacillus thermoglucosdasius useful for decomposing hydrogen peroxide in residual disinfectant remaining on
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                         Catalase; genetic engineering; hydrogen peroxide decomposition; contact lens; disinfectant.
                                                                                                                                                                               ö
                                                                                                                                                            Score 75; DB 21; Length 512; Pred. No. 0.0056;
                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                          Bacillus thermoglucosidasius catalase kat 19 SEQ ID NO:9.
                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 25-28; 30pp; English.
                                                                                                                                                                                                                                                                  AAY78358 standard; Protein; 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOT-) DEV CENT BIOTECHNOLOGY.
                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                  99US-0160981.
99US-0160989.
99US-0161404.
                                                                        99US-0161406.
99US-0161359.
99US-0161360.
       99US-0160814.
99US-0160815.
99US-0160980.
                                                                                                                                                                                                                                                                                                                                                                       Bacillus thermoglucosidasius
                                                                                                                                                                                                                                                                                                                                                                                                                                                97TW-0100018.
97CN-0120386.
                                                                                                   99US-0161361.
99US-0161920.
99US-0161992.
                                                                                                                                                            47.8%; 61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0027166.
                                                                                                                                99US-0161993
99US-0162142
                                                                                                                                                                                                                                                                                                       05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lo C, Chang LE;
                                                                                                                                                                     Local Similarity 61.9
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160378/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ88398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact lens
                                 22-071-1999
25-071-1999
25-071-1999
25-071-1999
26-071-1999
26-071-1999
28-071-1999
28-071-1999
                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                         US6022721-A.
                                                                                                                                         29-OCT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                           08-FEB-2000
                           22-OCT-1999
                                                                                                                                28-OCT-1999
                                                                                                                                                                                                                                                                                     AAY78358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hwong C,
                                                                                                                                                              Query Match
                                                                                                                                                                               Matches
g
                                                                                                                                                                                                                                                                                     ò
```

```
ó
                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                   Gaps
                                 ö
 DB 21; Length 483;
                                 5; Indels
Score 71; DB 21
Pred. No. 0.021;
                                                                                                                                                                                                                                                                                      Zea mays protein fragment SEQ ID NO: 20715.
                                   4; Mismatches
                                                                                                                                                                                     AAG19059 standard; Protein; 115 AA.
                                                                  7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                      | ||::|||| |: ||:|| || 5 klttswgapvgdnqnsmtagsrg 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0137222.
99US-0137528.
99US-0137502.
 45.28;
                 60.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0130077
99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0130510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0131449
99US-0132048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0132484
99US-0132485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0134218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0134370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0125788
99US-0126264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0128714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0130891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0132486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0132863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0134768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0135353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0135629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0128234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0132407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0132487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0135124
                                                                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134
```

90S-0137724 90S-0138040 90S-0138847 90S-0139119 90S-01391452 90S-0139452 90S-0139455 90S-0139455 90S-0139456 90S-0139456 90S-0139456 90S-0139456 90S-0139456	9050139461 9050139462 9050139463 9050139750 9050139899 9050140854 9050140854 9050141842 9050141842 905014280 905014280 905014280 905014280 9050143624 9050144985 9050144985 9050144985 9050144985 9050144985 9050144985 9050144985 9050144985 9050144985	8
8-70N-1999 8-70N-1999 9-70N-1999 9-70N-1999 9-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999 8-70N-1999	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	9 - JUL - OU -
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	X X X X X X X X X X X X X X X X X X X	***************************************

PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147433.
PR 10-AUG-1999; 99US-0147433.
PR 11-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148131.
PR 11-AUG-1999; 99US-0148131.
PR 11-AUG-1999; 99US-0148131.
PR 11-AUG-1999; 99US-0148131.
PR 20-AUG-1999; 99US-0148131.
PR 20-AUG-1999; 99US-0149122.
PR 20-AUG-1999; 99US-0149123.
PR 20-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-015106.
PR 28-ESP-1999; 99US-015106.
PR 28-ESP-1999; 99US-015106.
PR 28-ESP-1999; 99US-015106.
PR 28-ESP-1999; 99US-015106.
PR 29-ESP-1999; 99US-015106.
PR 29-ESP-1999; 99US-015106.
PR 21-CCT-1999; 99US-015029.
PR 21-CCT-1999;

ö

Gaps

ó

Score 70; DB 21; Length 115; Pred. No. 0.006; 4; Mismatches 5; Indels

Query Match 44.6%; Best Local Similarity 57.1%; Matches 12; Conservative

```
990S-0139492.
990S-0139454.
990S-0139455.
990S-0139457.
990S-0139458.
990S-0139460.
990S-0139461.
990S-0139462.
990S-0139462.
990S-0139462.
990S-0139462.
                                                                                                                                                                                                                                                                                                                                         9905 - 0142803
9905 - 0142803
9905 - 0143242
9905 - 0143542
9905 - 0144005
9905 - 0144006
9905 - 0144331
9905 - 0144333
9905 - 0144333
9905 - 0144333
9905 - 0144333
9905 - 0144334
9905 - 0144335
9905 - 0144335
9905 - 0144634
9905 - 014508
9905 - 0145192
9905 - 0145192
9905 - 0145192
9905 - 0145193
9905 - 0145193
9905 - 0145193
9905 - 0145193
9905 - 0145193
9905 - 0145193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0145951
990S-0146386
990S-0146389
990S-0146389
990S-0147038
990S-0147204
990S-0147192
990S-0147192
990S-0147416
990S-0147416
990S-0148171
990S-0148171
990S-0148171
                                                                                                                                                                                                     990S-0140353.
990S-0140354.
990S-0140695.
990S-0140823.
990S-0140991.
                                                                                                                                                                                                                                                                                     99US-0141842.
99US-0142154.
99US-0142055.
99US-0142390.
117-70N-1999;
18-70N-1999;
18-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 - JUL - 1999

02 - AUG - 1999

02 - AUG - 1999

03 - AUG - 1999

04 - AUG - 1999

05 - AUG - 1999

05 - AUG - 1999

06 - AUG - 1999

06 - AUG - 1999

09 - AUG - 1999

10 - AUG - 1999
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 33331.
                                                                                                       AAG28201 standard; Protein; 492 AA
            TTAFGAPVWDDNNVITAGPRG 29
|| || || || || || || || || || || ttnsgapvwnnnsaltvgqrg 38
                                                                                                                                                                                                                                                                                                                                                                            990S - 0121825 . 999S - 0121825 . 999S - 0123180 . 999S - 0125788 . 999S - 0125788 . 999S - 0125788 . 999S - 0125785 . 999S - 0132485 . 999S - 0132485 . 999S - 0132486 . 999S - 0132486 . 999S - 0132487 . 999S - 0132487 . 999S - 0134218 . 999S - 0134218 . 999S - 0134218 . 999S - 0134219 . 999S - 01342219 . 999S - 0135529 . 999S - 0135529 . 999S - 0135529 . 999S - 013724 . 999S - 013724 . 999S - 013724 . 999S - 013724 . 999S - 013722 . 999S - 013722 . 999S - 013724 . 999S - 013724 . 999S - 0139453 .
                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000; 2000EP-0301439
                                                                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1999

05-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

16-APR-1999

13-APR-1999

13-APR-1999

13-APR-1999

13-APR-1999

13-APR-1999

14-MAY-1999

19-MAY-1999

19-MAY-1999

25-MAY-1999

26-MAY-1999

27-MAY-1999

28-MAY-1999

28-MAY-1999
                                                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
16-JUN-4999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                  AAG28201;
                                                                               16
            σ
                                    18
                                                                                           AAG28201
              ŏ
                                   g
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 33330.
AAG28200

LD AAG28200

XX

XX

AG28200;

XX

T)-CCT-2000 (first entry)

XX

Arabidopsis thaliana protein fragment

XX

Arabidopsis thaliana protein fragment

XX

Commination sequence.

XX

Arabidopsis thaliana.

YX

Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%; Score 68; DB 21; Length 492; 57.1%; Pred. No. 0.063; ive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||||||:||: || || || ttnsgapvwnnnssltvgtrg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9905 - 0151438
9905 - 0151438
9905 - 0153930
9905 - 0153070
9905 - 0153070
9905 - 0154018
9905 - 0154018
9905 - 0154018
9905 - 0155139
9905 - 0155139
9905 - 0155139
9905 - 015923
9905 - 015923
9905 - 015923
9905 - 015923
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015933
9905 - 015963
9905 - 015963
9905 - 015963
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 016076
9905 - 0161405
9905 - 016136
9905 - 016136
9905 - 016136
9905 - 016136
                                   990S - 0149368
990S - 0149368
990S - 0149426
990S - 0149723
990S - 0149929
990S - 0149929
990S - 0149929
990S - 0149930
990S - 0150884
990S - 0151065
990S - 0151065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
Les 12; Conserv
   13-AUG-1999;
16-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
30-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15. SEP - 1999

20. SEP - 1999

24. SEP - 1999

24. SEP - 1999

25. SEP - 1999

26. SEP - 1999

27. SEP - 1999

28. SEP - 1999

29. SEP - 1999

20. SEP - 1999

20. SEP - 1999

20. SEP - 1999

21. SEP - 1999

22. SEP - 1999

23. SEP - 1999

24. SEP - 1999

25. SEP - 1999

26. SEP - 1999

27. SEP - 1999

28. SEP - 1999

29. SEP - 1999

29. SEP - 1999

20. SEP - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
```

ò g

```
PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0133462.

PR 18-JUN-1999; 99US-0133462.

PR 18-JUN-1999; 99US-0133462.

PR 23-JUN-1999; 99US-0133763.

PR 23-JUN-1999; 99US-0139763.

PR 23-JUN-1999; 99US-0139763.

PR 23-JUN-1999; 99US-0139763.

PR 23-JUN-1999; 99US-0140323.

PR 23-JUN-1999; 99US-0140323.

PR 23-JUN-1999; 99US-014220.

PR 13-JUL-1999; 99US-014433.

PR 13-JUL-1999; 99US-014433.

PR 22-JUL-1999; 99US-014433.

PR 23-JUL-1999; 99US-014
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 43.3%; Score 68; DB 21; Length 536; Best Local Similarity 57.1%; Pred. No. 0.069; Matches 12; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide; 15
990S - 0149902 - 990S - 0149930 - 990S - 015056 - 990S - 015068 - 990S - 0151065 - 990S - 015108 - 990S - 015659 - 990S - 015659 - 990S - 015659 - 990S - 0157117 - 990S - 0157753 - 990S - 0157752 - 990S - 990S - 0157752 - 990S - 0157752 - 990S - 0157752 - 990S - 015775
                                                                                                                                                                                                                                                                                                                                                                                                                                                       990S-0158232.
990S-0158369.
990S-0159293.
990S-0159294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0159638.
99US-0159584.
99US-0160741.
99US-0160767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0159329.
990S-0159330.
990S-0159331.
990S-0159637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161404.
99US-0161405.
99US-0161406.
                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0157865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0160770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0160981
99US-0160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0160815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0160980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |||||::|::| || ||
ttnsgapvwnnnssltvgtrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW40233 standard;
23-AuG-1999;
25-AuG-1999;
25-AuG-1999;
27-AuG-1999;
37-AuG-1999;
37-AuG-1999;
31-AuG-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
33-SEP-1999;
34-SEP-1999;
34-SEP-1999;
34-CCT-1999;
34-CCT-1999;
34-CCT-1999;
34-CCT-1999;
35-CCT-1999;
35-CCT-1999;
36-CCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW40233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW40233
ID AAW4
XX AC AAW4
XX DT 08-J
     Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for cencide proteins. They are useful for genemic DNA predicted to encode proteins. They are useful for genemic DNA predicted to expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The resent sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #3121 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                            claim 27; SEQ ID NO 13415; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 22;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB35615 standard; Peptide; 57
                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
30-JUN-2000; 2000US-0608408.
03-MGC-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234589.
27-SEP-2000; 2000US-0236389.
                                                                            2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe of the invention.
                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                             WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000; 26-MAY-2000; 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens,
                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB35615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB35615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW40229-W40247 are the N-terminal peptide fragments from various membrane proteins or membrane associated proteins isolated from Helicobacter pylori. Such N-terminal fragments could be used for therapeutic or diagnostic purposes, especially for developing vaccines against H. pylori infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #3098 encoded by breast cell single exon nucleic acid probe.
                                      Membrane protein; membrane associated protein; therapy; diagnostic;
vaccines; infection; adhesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori membrane proteins – useful for production of vaccines and antibodies for therapeutic and diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 19; Length 15;
Pred. No. 0.0017;
); Mismatches 1; Indels
H. pylori 63 kD adhesin N-terminal fragment.
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB30447 standard; Peptide; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON BEHRING GMBH & CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 9; 20pp; German.
                                                                                                                                                                                                               /label= unknown
                                                                                                                                                                         label- unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.78;
92.98;
                                                                                                                                                                                                                                                                                                                                                                    96DE-1030390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                                                                                              96DE-1030390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 vnkdvkqtxafgap 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VNKDVKQTTAFGAP 15
                                                                                              Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-102017/10
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hundt E, Knapp B,
                                                                                                                                                                                           Misc-difference 10
                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157271-A2.
                                                                                                                                                                                                                                                 DE19630390-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                            26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1996;
                                                                                                                                                                                                                                                                                        29-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB30447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
```

19

g ò

ö

Gaps

ö

Length 57; 7; Indels

```
Human; brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483446/52
                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy; cancer.
                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                        Claim 15;
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                             AAM56432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
            Single
hearts
                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                 AAM56432
    셤
                                                                                                                                                                                                                                                                                                                                                                         δŻ
                                                                                                                                                                                                                                                                                                                                    NX SX N
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein #3043 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                     Claim 27; SEQ ID NO 28250; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                   22; Length 57;
                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                  Score 66; DB 22
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                    ·;
                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                         ABB21044 standard; Protein; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                  || | || | || || || || || || || || ttgagnpvgdklnvitvgprg 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456.
2000US-0608408.
2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                 42.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                      Conservative
                                                                   DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                     WPI; 2001-483447/52
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488899/53
                                                                   Hanzel
                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157274-A2
                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                            ABB21044;
                                                                                                                                                                                                                                                       Sequence
                                                                   SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                   Penn
                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                                                                                           9
 õ
                                                                                                                                                                                                                                                                                                                                          g
```

```
ö
                                                                                                                                                                              measuring human gene expression in a sample derived from human heart (see ABA21335-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 28537.
exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                       The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 28537; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 22; Length 57; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                         SEQ ID No 22814; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM56432 standard; Protein; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
```

TTAFGAPVWDDNNVITAGPRG

```
à
                                                                                                                                                                     ö
probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow expressed exon; gene expression analysis; probe;
ray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed probe encoded protein SEQ ID NO: 29119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO: 29119; 658pp + Sequence Listing; English.
                                                                                                                                                                     ö
                                                                                                                                          57;
                                                                                                                                                                     7; Indels
                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyzing gene expression in human bone marrow
                                                                                                                                          DB 22;
0.011;
                                                                                                                                                                     Mismatches
                                                                                                                                          Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR,
                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                  ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                        AAM68813 standard; Protein; 57
                                                                                                                                                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                          42.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0024263
                                                                                                                                                                                                TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                               (first entry)
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488900/53.
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157276-A2
                                                                                                   23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                              06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                 microarray;
                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                    AAM68813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                        9
                                                                                                                                                                     Matches
                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                    8888888888
                                                                                                                                                                                                à
```

```
The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPS are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer. Once: The square did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                  Peptide #3065 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful fanalyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 22;
Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID No 21457; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                         ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM29117 standard; Protein; 57
                                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
  26
                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                         AAM16631 standard; Protein;
                                                                                                                                                                                                                                                                                        2001WO-US00670
                                                                                                                                                                                                                                                                                                                            2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.78;
                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0024263
|| | || | || || || || || || || || ttgagnpvgdklnvitvgprg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä,
                                                                                                                                                                                         cervical cancer
                                                                                                                                                                                                                                       WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 21-SEP-2000; 27-SEP-2000;
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2000;
                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG,
                                                                                                 AAM16631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM29117
                                                                                      Ω×
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

ö

Gaps

ö

Score 66; DB 22; Length 57; Pred. No. 0.011; 0; Mismatches 7; Indels

42.0%;

Best Local Similarity 66.7 Matches 14; Conservative

Query Match

Probe;

```
The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catalase; PCR; primer; amplification; expression; E.coli; decomposition; hydrogen peroxide; disinfectant; contact lens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 66; DB 22; Length 57;
Pred. No. 0.011;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus thermoglucosidasius catalase protein.
                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 13088; 322pp; English.
                                                                                                                                                                                                                      DR;
                                                                                                                                                                                                                    Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44174 standard; Protein; 483 AA.
                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thermoglucosidasius
              29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0055299.
                                                 2000US-0180312
                                                                                                                2000US-0234687
2000US-0236359
                                                                                                                                                   2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0055299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.77
                                                                                                                                                                                                                    Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                     WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                        in a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AA;
                                                                                                                  21-SEP-2000;
27-SEP-2000;
                                                                                30-JUN-2000;
03-AUG-2000;
                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP11243961-A.
                                                 04-FEB-2000;
                                                                  26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY44174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                               Peptide #3154 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #3030 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66; DB Pred. No. 0.013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID No 29386; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM04348 standard; Protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                  2000US-0632366.
2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%;
                                                                                                                                                                                                                                                                                                      2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00663
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 AA;
                                                                                                                  genetic disorder
                                                                                                                                                                                 WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157270-A2
                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                   26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-3001.
                             17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-0CT-2001
                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
AAM29117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM04348;
```

56

ò 셤

ö

Gaps

ö

ò 셤

```
polynucleotide which comprises the sequence (1) given in the specification. The invention also describes 1) a catalase polypeptide comprising at least residues 127 to 509 of the fully defined amino acid given in the specification, 2) a recombinant vector carrying comprising the gene; and 3) a transformant transformed by the above recombinant vector. The catalase is useful as an enzymatic agent decomposing hydrogen peroxide contained in waste water.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Vibrio rumoiensis S-1 catalase polypeptide and polynucleotide for treating waste water -
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel Vibrio rumoiensis S-1 catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Length 509;
                                                                                     Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase; hydrogen peroxide decomposition; waste water.
                                                                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
.
                                                                                   DB 21;
0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 66; DB 2;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                    V. rumoiensis S-1 catalase protein SEQ ID 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                      3; Mismatches
                                                                                     Score 66;
Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥.
                                                                                                                                                                                                                                                                                          ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 7-8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                          AAB46776 standard; Protein; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP82004 standard; protein; 527
                                                                                                                                                              7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                              5 klttswgapvgdnqnsitagnpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%;
61.9%;
                                                                                   Query Match
Best Local Similarity 60.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0134831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0134831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || ||||| :::|||||||
|4 ttdfgapvvtnrdsltagprg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-106416/12.
N-PSDB; AAF25916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio rumoiensis.
                                  483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2000316584-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                  19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP82004;
                                  Sequence
                                                                                                                                                                                                                                                                                                                                AAB46776;
   enzyme.
                                                                                                                                                                                                                                                       59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                          AAB46776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP82004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                              XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
SXS
                                                                                                                                                                δ
                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a catalase isolated from Bacillus thermoglucosidasius. A composition containing a B. thermoglucosidasius catalase is used to decompose hydrogen peroxide present in residual disinfectant remaining on a contact lens to avoid undesired injury to users. The catalase enzyme can also be used to treat textile substances which have been bleached with hydrogen peroxide. The catalase is derived from a non-mammalian source and reducing the need to use boyine liver catalases so the risk of cross infection from cows to humans is reduced. The production procedure is simple and has low cost with high yield of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated catalase gene derived from Bacillus thermoglucosdasius useful for decomposing hydrogen peroxide in residual disinfectant remaining on a contact lens -
                                                                                                                                         This sequence corresponds to the catalase protein (kat 19) from the microorganism Bacillus thermoglucosidasius. The gene was PCR amplified and inserted into the plasmid pET-20b for expression in an organism such as E.coli DH5alpha. The protein can be used for the decomposition of hydrogen peroxide contained in the residual disinfectant remaining in a contact lens solution.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                   Preparation of catalase - useful for production of catalase in high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Catalase; genetic engineering; hydrogen peroxide decomposition; contact lens; disinfectant.
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                              Score 66; DB 20; Length 483;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thermoglucosidasius catalase kat TG SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                    ;
9
                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78357 standard; Protein; 483 AA.
                                                                                                        Page 3; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                     5 klttswgapvgdnqnsitagnpg 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Fig 6; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    7 KOTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOT-) DEV CENT BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                              42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thermoglucosidasius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97TW-0100018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0027166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-160378/14.
N-PSDB; AAZ88397.
WPI; 1999-603710/52
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                         483 AA;
                 N-PSDB; AAZ28794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               လ
လ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-1997;
11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6022721-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78357;
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hwong C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 28
                                                                      yield
                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78357
```

A STATE OF S

```
Biochemical markers of human endometrium - useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BETA-) BETAGENE INC.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimabukurom,
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human catalase sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hohmeier H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-153448/13.
N-PSDB; AAX08433.
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                            527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9906059-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark SA,
Ohneda M,
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW96321;
                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW96321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The DNA encoding the gene can be used to produce recombinant catalase which, with superoxide dismutase, is an important anti-
inflammatory factor in vivo and can be used as a drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                  used to produce catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9;
                                                                   Catalase; inflammation; antiinflammatory drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.0%; Score 66;
66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CLIN-) CENT CLINICAL & BASIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW54361 standard; protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larsen P;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1; 5pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                             (MITK ) MITSUI TOATSU CHEM IND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                          86JP-0159690.
                                                                                                                                                                                                        86JP-0159690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-GB02394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-0007132
96GB-0018600
                                                                                                                                                                                                                                                                                                                                                                                   for antiinflammatory drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || | || || |||| |||| ||||| 28 ttgagnpvgdklnvitvgprg
15-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fey SJ,
                                  Recombinant catalase
                                                                                                                                                                                                                                                                                                            WPI; 1988-061234/09.
N-PSDB; AAN82012.
                                                                                                                                                                                                                                                                                                                                                                Human catalase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-207057/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAN82011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Byrjalsen I,
                                                                                                                                      JP63017693-A
                                                                                                    Homo sapiens
                                                                                                                                                                                                        06-JUL-1986;
                                                                                                                                                                                                                                          06-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9810291-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1997;
                                                                                                                                                                         25-JAN-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW54361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW54361
NOT COURT OF STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

6

```
endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of call lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or neurodegenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes mellitus; treatment; therapy; nitric oxide; NO; beta cell; fatty acid; lipotoxic; cytotoxic; cytokine; osteoporosis; inflammatory disease; autoimmune disease; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibition of cytokine mediated immunotoxicity of cells can be achieved by blocking free radical production or the accumulation of free radicals in that cell. Treatment of insulin dependent diabetes mellitus (IDDM) can be achieved by blocking nitric oxide (NO) production in a pancreatic beta cell and by providing a composition comprising an agent that reduces levels of fatty acids in the cells
                                                                                                                                                          Proteins AAW54349-W54364 are examples of proteins produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manganese containing superoxide dismutase; MnSOD; IDDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee Y, New
A, Unger RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 19
Pred. No. 0.14;
0; Mismatches
                        diagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 242-244; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koyama K, Le
, Thigpen A,
                                                                                            Disclosure; Page 23; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96321 standard; Protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US15781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0055092
97US-0055092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAFGAPVWDDNNVITAGPRG
```

ö

Gaps

ö

à

```
production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity. Infinity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                       Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; current nervous system; cNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F,
                                                                                                                                                                                                                           22; Length 527;
                                                                                                                                                                                                                                                      7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         en R, Ma Y, (
u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                     0.14;
                                                                                                                                                                                                                         Score 66; DB 2
Pred. No. 0.14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 3013; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen R,
                                                                                                                                                                                                                                                                                                                                                                                 AAM39868 standard; Protein; 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 3013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Asundi V, Chen
Liu C, Wehrman T, Xu
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                         42.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0488725.
2000US-0552317.
2000US-059842.
2000US-0620312.
2000US-0653450.
2000US-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2000; 2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0727344
                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47.
N-PSDB; AAI59024.
                                                                                                                                                                                                                                       Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                               527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2000; 29-JUL-2000; 219-JUL-2000; 203-AUG-2000; 214-SEP-2000; 29-NOV-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OA,
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               AAM39868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2hao
                                                                                                                                                                                                                                                                                                                                                                     AAM39868
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                  888888888888888
                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ψa
                   death. Cells can also be protected against nitric oxide mediated cytotoxicity by introducing into the cell an antioxidising agent. The methods can be used for protecting cells against immunotoxicity mediated by, e.g. IL-1 beta, IL-1 alpha, gamma IFN, TNF alpha, TNF beta, IL-8, IL-7, IL-7, IL-7, IL-7, IL-19, IL-14, IL-17, granulocyte-macrophage colony stimulating factor or monocyte chemoattractant protein-1. The methods can be used for the treatment of e.g. insulin-dependent diabetes mellitus (IDDM), NIDDM, obesity, wasting syndromes, short stature, osteoporosis, inflammatory diseases, autoimmune diseases, or neurodegenerative diseases.
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
        protects beta-cells of the subject against lipid-mediated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang ZW;
                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                      42.0%; Score 66; DB 20; Length 527; 66.7%; Pred. No. 0.14; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u P, Xu C,
Chen R, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang J, Ren F, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; Page 3328-3329; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAM78440 standard; Protein; 527 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT,
Wang D, Wang J, Zhi
Yang Y, Wejhrman T,
                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                 || | || | || || || || || || || || ttgagnpvgdklnvitvgprg 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein SEQ ID NO 1102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0496914.
2000US-0560875.
2000US-06298075.
2000US-06298075.
2000US-0654936.
2000US-0653551.
2000US-0693325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-476283/51.
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                              527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAK51573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001,
                                                                                                                                                                                                                                     Best Local Sim
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Zhao QA,
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              AAM78440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tue AJ,
                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                    AAM78440
                                                                                                                                                                                                                                                                                                                                                       RESULT
        8
```

ä

Wang

```
ö
the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, chemotractic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                         The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hackneistic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, War
                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                               DB 22; Length 527;
0.14;
ches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                               42.0%; Score 66; DB 66.7%; Pred. No. 0.14 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, us such as _{\rm j}{\rm central} nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 6585.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM41654 standard; Protein; 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Asundi V, Che
Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
                                                                                                                                                                                                                                                                                                                                          9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                           2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0488725
2000US-0552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0653450.
2000US-0662191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0598042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0693036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
N-PSDB; AAI60810.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                            C.N.S disorders
                                                                                                                                                                                                                                       527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
                                                                                                                                                                                                          specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OA,
                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM41654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΥT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                               AAM41654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
   ð
```

```
The invention relates to human nucleic acids (AAL57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Anhibin activity, chemctactic/chemckinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ma Y;
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                22; Length 558;
                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                              Score 66; DB 22
Pred. No. 0.15;
0; Mismatches
           Example 2; SEQ ID NO 6585; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM79424 standard; Protein; 565
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                        Human protein SEQ ID NO 3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                                                                                                              42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                             Query Match 42.0
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAK52557
                                                                                                                                                                                                                            .N.S disorders.
                                                                                                                                                                                                                                                                                      558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157190-A2
                                                                                                                                                                                                                                                        specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-2000;
20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM79424;
                                                                                                                                                                                                                                                                                        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM79424
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
a
```

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                 The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetical and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                              Inframmetton.

MAKE: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a wheat catalase gene which is inserted in a rice genome in order to improve cold-resistance. Such a cold-resistant catalase is useful for the decomposition of hydrogen peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene - useful for producing
the decomposition of hydrogen
Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catalase; rice; wheat; plant; cold-resistance; hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 2;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOKK-) HOKKAIDO GREEN BIO KENKYUSHO KK.
                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice having cold-resistance catalase cold-resistant rice and catalase for peroxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOKU-) HOKUREN NOGYO KYODO KUMIAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 12; 17pp; Japanese.
                                                                                6221pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW63845 standard; Protein; 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-0086029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96JP-0090382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 ttgagnpvgdklnvitvgprg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                Claim 20; Page 242-243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wheat catalase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-430953/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV44050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             decomposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP10179167-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW63845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

ò g

```
The present sequence is a rat mitogenic oxidase mox1B
which is capable of stimulating production of superoxide, a reactive
oxygen intermediate (ROI) that affects cell division. The present
sequence was obtained from a rat convalidation. The present
sequence was obtained from a rat convalidation. The present
cells exposed to angiotensin II. Mox1B is a spliced variant of rat mox1,
also referred as p65mox. The mox1B protein functions as a mitogenic
regulator. The present sequence is useful in developing
regulator. The present sequence is useful in developing
regulator. The present sequence is useful in developing
growth, including cancer, psoriasis, prostatic hypertrophy, benign
prostatic hypertrophy, cardiovascular disease, proliferation of vessels,
c s.g. blood vessels and lymphatic vessels, arteriovenous malformation,
vascular problems associated with eye, atherosclerosis, hypertension,
and restenosis following angioplasty.
                                ö
                                                                                                                                                                                                                                                                                                                      Rat; mitogenic regulator; mox1B; mitogenic oxidase; p65mox; superoxide; reactive oxygen intermediate; RoI; cell division: cytostatic; antipsoriatic; cardiant; antiarteriosclerotic; vasotropic; antiangiogenic; hypotensive; drug development; treatment; cancer; abnormal growth; psoriasis; prostatic hypertrophy; proliferation; blood vessel; lymphatic vessel; benign prostatic hypertrophy; cardiovascular disease arteriovenous malformation; eye disorder; hypertension; atherosclerosis; restenosis; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guangjie C;
                                ö
DB 19; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arnold RS,
                                5,
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griendling KK,
Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 120-122; 141pp; English.
                                                                                                                                                                                        AAY71122 standard; Protein; 499 AA.
                                                                  29
                                                                                                                                                                                                                                                                                             Rat mitogenic regulator mox1B.
                                                                                                   38
40.8%;
52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107911.
99US-0149332.
99US-0151242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US26592.
                                                                                        9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lassegue BP,
                                11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376545/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMORY.
              Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD00695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200028031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYEM-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lambeth JD,
                                                                                                                                                                                                                                                           08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
                                                                                                                                                                                                                        AAY71122;
 Query Match
                                                                                                                                                       38
```

Length 499;

DB 21;

38.9%; Score 61;

A.

499

Sequence

Query Match

1;

Gaps

7

Indels

5,

7; Mismatches

28

셤

ã

```
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               DE19820190-A1
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-APR-1998;
                                                                                                                                                                                                                                                         14-MAR-2000
                                                                                                                                                                                                                                                                                                                                    Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23;
                                                                                                                                                                                                                                                                                                                                                        treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                   AAY73954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins
                                                                                                                                        40
       Matches
                                                                                                                                                            AAY73954
                                                                                                                                      RESULT
                                                                             g
                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also referred as p65mox, which is capable of stimulating production of superoxide, a reactive oxygen intermediate (ROI) that affects cell division. The present sequence was obtained from a rat aortic smooth muscle cell. The moxl protein functions as a mitogenic regulator and shows homology to human moxl protein. It is expressed in aortic smooth muscle cells and induced by angiotensin II, platelet-derived growth factor (PDGF) and phorbol myristic acid (PMA).

The present sequence is useful in developing drugs and therapies for treatment of conditions associated with abnormal growth, including cancer, psoriasis, prostatic hypertrophy, benign prostatic hypertrophy, cardiovascular disease, proliferation of vessels e.g. blood vessels and lymphatic vessels, arteriovenous malformation, was cular problems associated with eye, atherosclerosis, hypertension,
                                                                                                                                                                                                                                                                                                                                                Rat; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide; reactive oxygen intermediate; R01; cell division; cytostatic; antipsoriatic; candiant; antiarteriosclerotic; vasotropic; antiangiogenic; hypotensive; drug development; treatment; cancer; abnormal growth; psoriasis; prostatic hypertrophy; proliferation; blood vessel; lymphattc vessel; benign prostatic hypertrophy; cardiovascular disease; arteriovenous malformation; eye disorder; hypertension; atherosclerosis; restenosis; angioplasty.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guangjie C;
                       ä
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arnold RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a rat mitogenic oxidase mox1,
                       5;
   44.0%; Pred. No. 0.75;
tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griendling KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 98-100; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and restenosis following angioplasty
                                                                                 :|| |:|| |:||: : : || |:
434 lkqktsfgrpmwdnefsriatahpk 458
                                                           6 VKQTTAFGAPVWDD--NNVITAGPR 28
                                                                                                                                                                                             AAY71121 standard; Protein; 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0107911.
99US-0149332.
99US-0151242.
                                                                                                                                                                                                                                                                                                              Rat mitogenic regulator mox1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26592.
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lassegue BP,
Best Local Similarity 44.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-376545/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYEM-) UNIV EMORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD00694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200028031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1999;
                                                                                                                                                                                                                                                                         08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lambeth JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus sp.
                                                                                                                                                                                                                                   AAY71121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
```

Score 61; DB 21; Length 563; Pred. No. 0.86;

38.9%;

Query Match Best Lącal Şimilarity

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel polypeptides and their encoding nucleic acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAY73814-Y74252 represent protein fragments encoded by the human pancreatic tumor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library derived expressed sequence tag (EST) sequences represented in AAS28888-253014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dahl
                                                                                                                                                                                                                                                                                                                                                                            tumor; EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                            Human prostate tumor EST fragment derived protein #141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.9%; Score 58; DB 20;
45.0%; Pred. No. 0.55;
tive 5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 22, 2002, 07:44:07 Job time: 66 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hinzmann B,
                                                                                                                                                                            AAY73954 standard; Protein; 152 AA
                                                522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 368; 502pp; German
6 VKQTTAFGAPVWDD--NNVITAGPR :|| |:|| |:|| |: || |: || || 498 lkqktsfgrpmwdnefsriatahpk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 QTTAFGAPVWDDNNVITAGP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98DE-1020190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98DE-1020190
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-621386/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ52904
```

Š

```
US-08-553-633A-2
US-08-737-825-2
US-07-857-224B-21
US-07-857-224B-21
US-09-230-6319-15
US-09-230-637-31
US-08-713-828-3
US-08-713-828-3
US-08-713-828-4
US-08-713-828-5
US-08-713-828-5
US-08-713-828-5
US-08-713-828-5
US-08-713-828-5
US-08-713-828-5
US-09-113-828-5
US-09-113-828-5
US-09-113-828-5
US-09-113-828-5
US-09-113-828-5
US-09-118-324-5
US-09-118-334-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-108-262-2
US-08-961-083-22
US-08-615-942A-2
US-08-935-760-2
US-08-559-397A-19
                                                                                                                                                                                                                                                                                US-08-446-100-18
US-08-446-100-24
US-09-334-489-3
US-09-334-489-4
5215909-11
US-08-952-127-12
US-09-082-737-5
US-09-08-737-5
US-09-08-737-5
US-09-08-737-5
US-09-965-138-12
US-08-559-397A-31
US-08-955-138-12
US-08-955-138-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-852-743-3
US-09-185-370-3
US-09-419-459-4
US-09-414-555A-2
US-08-559-397A-2
         US-08-689-411-2
PCT-US94-09863-2
US-08-407-229-2
US-08-446-100-1
US-08-446-100-3
US-08-446-100-4
US-08-446-100-4
US-08-446-100-6
US-08-446-100-6
US-08-446-100-7
US-08-446-100-7
US-08-446-100-7
US-08-446-100-7
US-08-446-100-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-475-682-2
US-08-780-833-2
US-08-636-036-2
                                                                                                                                                                                                                                                     US-08-446-100-16
US-08-446-100-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-946-026-30
                                                                                                                                                                            US-08-446-100-11
US-08-446-100-12
                                                                                                                                                                                                         US-08-446-100-13
US-08-446-100-14
US-08-446-100-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-369-780-2
                                                                                                                                                                                                                                                                                                                                               602
3066
251
273
273
694
1183
450
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2568
3390
3394
4655
506
506
506
506
506
506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               471
492
492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643
109
268
42.5
42.5
42.5
42.5
41.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 21.52 Seconds (without alignments) 32.916 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptcdata/2/jaa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptcdata/2/jaa/PcTUS_COMB.pep:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.08-980-241.5

5.08-980-241.5

5.08-980-342-26

5.07-846-181-5

5.07-845-989-5

5.07-845-989-5

5.09-061-768A-2

5.09-185-370-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-704-711A-22
-08-448-489-11
-08-464-052-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-08-695-987-2
5-08-695-987-6
5-09-027-166-9
5-09-027-166-7
5-09-126-109-10
                                                                                                                                                                                                                                                                                                 hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -08-657-868B-4
-08-657-868B-5
-08-657-868B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -08-689-411-8
-08-464-052-4
-08-461-002-4
                                                                                                                                                                                            MVNKDVKQTTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-689-411-4
                                                                                                                                                                                                                                                                     231628 segs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                        - protein search, using sw model
                                                                                                     2002, 07:44:32
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
                                                                                                                                                                 US-09-488-737-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
483
483
527
527
527
730
730
730
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
2009
2009
2009
44
88
48
88
48
88
48
88
48
88
48
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                     August 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

4444

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.
97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
                                                                                                                                                                                                                                                                                                     Potal number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.5
52.5
52.5
50
44
50
44.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157
1157
1157
1157
73
73
71
66
66
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                 Minimum DB :
Maximum DB :
                                                                          protein
                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                      :
oo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
```

Sequence 2, Applisequence 2, Applisequence 1, Applisequence 1, Applisequence 2, Applisequence 1, Applisequence 6, Applisequence 7, Applisequence 12, Applisequence 13, Applisequence 13, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 2, Applisequence 3, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 3, Applisequence 2, Applisequence 4, Applisequence 5, Applisequence 6, Applisequence 6, Applisequence 6, Applisequence 12, Applisequence 13, Applisequence 14, Applisequence 14, Applisequence 15, A

Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

19,

Sequence 2 Sequence 2 Sequence 2 Sequence 2

Appli

Sequence 4, 1 Sequence 47, Sequence 47, Sequence 6, STREET: 130 Water Street

```
Query Match 100.0%; Score 157; DB 3; Length 505; Best Local Similarity 100.0%; Pred. No. 5.4e-17; Matches 29; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SUGIYAMA, TOSITO
APPLICANT: KAWABATA, Tomohisa
APPLICANT: HIRATSU, Kazunari
APPLICANT: HIRATSU, Kazunari
APPLICANT: HIRATSU, Takumi
ITTLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: BOSTON
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-ESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DISKETTE
OPERATING SYSTEM: DOS
SOFTWARE: FastESE for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,868B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08657868B Patent No. 6080556 GENERAL INFORMATION:
                                                                                                                                                                                                                                   FILING DATE: 31-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: 136465
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Reshick, David S
REGISTRATION NUMBER: 44,235
REFERENCE/DOCKET NUMBER: 4655
                                                                                                                                                                                                                                                                                                                                                                                                                                          1,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                         USA
Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                             02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-08-657-868B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-657-868B-4
                                         COUNTRY:
                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                         APPLICANT: DOING, Antian APPLICANT: LEC, Adrian APPLICANT: RADGLIFF, Fiona J. APPLICANT: RADGLIFF, Fiona J. APPLICANT: HAZELL, STUATL L. TITLE OF INVENTION: TREATHENT AND PREVENTION OF HELIOBACTER TITLE OF INVENTION: INFECTION NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREPT: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08657868B
Fatent No. 6080556
GEMERAL INFORMATION
GEMERAL INFORMATION;
APPLICANT: SUGITAMA, Tosiro
APPLICANT: HIRXASU, Kazunari
APPLICANT: TANAKA, Takumi
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION
ITILE OF INVENTION: AND USE
CORRESPONDENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCES: 1
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: Z0007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,987
FILING DATE: 15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 157; D
Best Local Similarity 100.0%; Pred. No. 5.4
Matches 29; Conservative 0; Mismatches
                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17227/128
                                                                                                                                                                                     DOIDGE, Christopher V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: BENY, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 17227
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)672-5300
TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
                                                                                                                       Sequence 4, Application US/08695987
Patent No. 6005090
GENERAL INFORMATION:
APPLICANT: DOIDGE, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-695-987-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-657-868B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
```

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DEE, Adrian
APPLICANT: RADCLIFF, Fiona J.
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES:
ADDRESSEE: FOLGY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 20007-5109

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,987
FILING DATE: 15-AUG-1996
CLASSIFICATION: 424
ATONINY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 153; DB 3; L
Pred. No. 2.4e-16;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                       ch 100.0%; Score 157; DB 3; Similarity 100.0%; Pred. No. 5.4e-17; 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                   1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17227/128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08695987
Patent No. 6005090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                                INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.5%;
Best Local Similarity 96.6%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-695-987-2
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                  US-08-657-868B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-08-695-987-2
                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: STGITAMA, TOSITO
APPLICANT: KAWABATA, TOMONISA
APPLICANT: HIRAYASU, KAZUNATI
APPLICANT: HIRAYASU, KAZUNATI
APPLICANT: TANAKA, TAKUMI
TITLE OF INVEWTION: POLYPEPTIDES, THEIR PRODUCTION
TITLE OF INVENTION: AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 157; DB 3; Best Local Similarity 100.0%; Pred. No. 5.4e-17; Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSER OF Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,868B
FILING DATE: 31-MAY-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136465
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: 83512
FILING DATE: 05-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08657868B
Patent No. 6080556
                                                                                                                                                                 NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 4652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 136465
FILING DATE: 02-JUN-1995
APPLICATION UNDBER: 83512
FILING DATE: 05-APR-1966
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
    FILING DATE: 31-MAY-1996
                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino ac
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-657-868B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-657-868B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
```

ð g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.2%; Score 71; DB 3; Length 483 60.9%; Pred. No. 0.0027; usematches 5; Indels
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ele POCOMPATIBLE
COMPUTER: ELEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,166
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
PRICH APPLICATION DATA:
APPLICATION NUMBER: TW 8610018
FILING DATE: 03-04N-1997
PRICH APPLICATION NUMBER: TW 8610018
FILING DATE: 11-DEC-1997
ATORNEY-AGENT INFORMATION:
NAME: CHAO, MATX
REGISTRATION NUMBER: 38,180
TELEPHONE: (312) 913-0002
INFORMATION FOR INFORMATION:
TELEPHONE: (312) 913-0002
INFORMATION FOR INFORMATION:
CONTINUENT (122) 913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: IL.
COUNTRY: USA
2 ID: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,166
FILING DATE: 20-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||::|||| |: |:|| || || 5 KLTTSWGAPVGDNQNSMTAGSRG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 KOTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I: 483 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein US-09-027-166-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
  Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicago
                                         USA
                                                          ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09027166

Sequence 9, Application US/09027166

Sequence 9, Application US/09027166

Sequence 9, Application US/09027166

Patent No. 6022721

APPLICANT: CHANG, Li-Yen Edward

APPLICANT: HWONG, Ching-Long

APPLICANT: HWONG, Ching-Long

TITLE OF INVENTION: No. 6022721e1 Catalase, The Gene Thereof and

TITLE OF INVENTION: Composition Comprising The Same, And Process For Preparing

TITLE OF INVENTION: Catalase Using Genetic Engineering Technology

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                            APPLICANT: DOING:
APPLICANT: LEE, Adrian
APPLICANT: LEE, Adrian
APPLICANT: RADCLIFF, Flona J.
APPLICANT: HAZELL, Stuart L.
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HELIOBACTER
TITLE OF INVENTION: 1NFECTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZITE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,987
FILING DATE: 15-ANG-1996
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: BENTY Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELEPRAK: (202)672-5300
TELEPRAK: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73; DB 3;
Pred. No. 2e-05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
RESULT 6
US-08-695-987-6
; Sequence 6, Application US/08695987
; Patent No. 6005090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVNKDVKQTTAFGAP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVNKDVKQTTAFGTP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-695-987-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
```

```
ö
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-365-486A-26
Sequence 26, Application US/08365486A
Sequence 26, Application US/08365486A
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                           42.0%; Score 66; DB 4; Length 527; 66.7%; Pred. No. 0.019; 1ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.3%; Score 57; DB 4; Length 495; 52.4%; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
               TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
WOLECULE TYPE: protein
US-09-126-109-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
   TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                       28 TTGAGNPVGDKLNVITVGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.3
Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                             Query Match 42.0
Best Local Similarity 66.7
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Nematodes
US-08-980-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94306
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-980-241-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                          Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Rudul, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TITLE OF INVENTION: TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 3;
Pred. No. 0.017;
3; Mismatches
                                                ATOR APPLICATION DATE:

APPLICATION NUMBER: CN 97120386.5
FILING DATE: 11-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: CHAO, MAIK
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 98,180
TELECHONIS: (312) 913-0001
TELEPAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-010-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNKNOWN
FILING DATE: 03-MAR-1998
ATTORNEY AGENT INFORMATION:
NAME: MCMILLian, Nabeela R.
REGISTRATION NUMBER: P-43,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: UTSD:560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Thigpen, Anice
APPLICANT: Hohmeler, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICATION NUMBER: TW 86100018 FILING DATE: 03-JAN-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09126109
Patent No. 6171856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                            42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.99
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-027-166-7
                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Texas
COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-126-109-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
```

á a

```
Gaps
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.4%; Score 52.5; DB 1; Length 730; 52.4%; Pred. No. 4; 1.1ve 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                            MESULT 13
US-07-846-181-5
Sequence 5, Application US/07846181
Patent No. 5360732
GENERAL INFORMATION:
APPLICANT: BERKA, RANDY M
APPLICANT: REX, MICHAEL W
TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENEROCY INTERNATIONAL, INC.
STREET: 180 KIMBALL WAY
CITY: SOUTH SAN FRANCISCO
STREET: CA
                                                                                                                                                       DB 4; Length 527;
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/846,181
FILING DATE: 19920304
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HORN MS, MARGARET A
REGISTRATION NUMBER: 33401
REFERENCE/POCKET UNBER: GC204-US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: 415-742-7336
                                                                                                                                                                                               3; Mismatches
                                                                                                                                                    35.7%; Score 56; 52.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/07845989; Patent No. 5360901; GENERAL INFORMATION:
                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                      28 TTGGNPIGDKLNIMTAGSRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
    : 527 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 730 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || || || : | : |||||| 59 TIDFGTPI-SDQTSLKAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-742-7217
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.49
                                                                                                                                                                                            Conservative
                                          TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-880-342-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-07-846-181-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                    Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-07-845-989-5
      LENGTH:
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ő
                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%; Score 56; DB 2; Length 527; 52.4%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/0880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Laderoute, Keith R.
APPLICANT: Laderoute, Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342

FILING DATE: 23-JUN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996

FILING DATE: 13-NOV-1995

PRIOR APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994

ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CURRAL.
APPLICATION ...
FILING DATE: 23-DE.
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38.615
REFERENCE/DOCKET NUMBER: 8255-0018
FELECOMMUNICATION INFORMATION:
FELECHONE: (415) 324-0860
FELEFAX: (415) 324-0860
FELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TVPE: Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sholtz, Charles K.
REGISTRATION UNDHER: 38,615
REFERENCE, TOCKET UNDER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 350 Cambridge Avenue, Suit CITY: Palo Alto STATE: CA COUNTY: USA 2IP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 TTGGGNPIGDKLNIMTAGSRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 324-0860
TELEFAX: (415) 334-0960
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.47
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-880-342-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-061-768A-2

Sequence 2, Application US/09061768A

Patent No. 6204037

GENERAL INFORMATION:

APPLICANT: BRASH, ALAN R.

APPLICANT: BRASH, MITSUO

TITLE OF INVENTION: LIFOXYGENASE PROTEINS AND NUCLEIC ACIDS

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADTRESS:

ADDRESSEE: ADTRESS:

CONTRES: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

CITY: DURHAM

STREET: SILTE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

COUNTRY: USA

ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: WINDOWS 3.1

COMPUTER: WORD PERFECT 6.1 and ASCII

COMPUTER: MORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA: US/09/061,768A

FILING DATE: APPLICATION DATA: NONE

APPLICATION NUMBER: US/09/061,768A

FILING DATE: APPLICATION DATA: NONE

APPLICATION NUMBER: REDADATION: A35

PRIOR APPLICATION DATA: NONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.8%; Score 50; DB 1; Length 1188; 47.4%; Pred. No. 18; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 4; Length 676;
Pred. No. 13;
                                                                                                                                                     P-UM 9783
                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryb A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM
TELECOMMUNICATION INFORMATION:
TELEFAN: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTOREY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFRENCE/DOCKET NUMBER: 1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.2%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 KOTTAFGAPVWDDNNVITA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 KNATAFHVTVQDDNNIVVS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 47.4 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-201-697-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08201697
Patent No. 5705623
GENERAL INFORMATION:
APPLICANT: Miggins, Roger C.
APPLICANT: Thomas, Peedikayil E.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
APPLICANT: BEEKA, RANDY M
APPLICANT: FOWLER, TIMOTHY
TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
TITLE OF INVENTION: CATALASE-R
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENEWATT
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: US/07/845,989
FILING DATE: 19920304
CLASSIFICATION NUMBER: US/07/845,989
FILING DATE: 19920304
CLASSIFICATION NUMBER: GC208-USI
REFERENCE/DOCKET NUMBER: GC208-USI
REFERENCE/DOCKET NUMBER: GC208-USI
TELEPHONE: 415-742-7217
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPIEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,697
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52.5; DB Pred. No. 4; 2; Mismatches
                                                                                                                                                                                                                                          ADDRESSEE: GENENCOR INTERNATIONAL, INC. STREET: 180 KIMBALL WAY CITY: SOUTH SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.4%;
Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-845-989-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-201-697-4
                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: Naxon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ć,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 44.5; DB 3;
33.3%; Pred. No. 23;
tive 6; Mismatches 9;
                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/327001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPRAX: 617/542-8906
    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/185,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DVKQTTAFGAPVWDDNNVITA---GPR 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/08689411; Patent No. 6224881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
                                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.3'
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-185-370-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 536
                                                                    CITY: DOC.
STATE: MA
COUNTRY: US
TP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-689-411-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
      Gaps
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ж
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.3%; Score 44.5; DB 2; Length 271; llarity 33.3%; Pred. No. 23; Conservative 6; Mismatches 9; Indels
      Indels
  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,743
FILING DATE: 7-MAY-1997
FILING DATE: 7-MAY-1997
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 60/016,774
FILING DATE: 7-MAY-1996
ATTORNEY-AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/POCKET NUMBER: 34,819
REFERENCE/POCKET NUMBER: 34,819
TELEPHONE: 617/442-8006
TELEPHONE: 617/442-8006
                                                                                                                                                                                                                                APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Force, Thomas
APPLICANT: Kyrlakis, John M.
APPLICANT: Kyrlakis, John M.
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
ALITLE OF INVENTION: SOK-1 AND METHODS OF USE
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 NIKRTTMVGTPYWMAPEVVSRKEYGPK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 DVKQTTAFGAPVWDDNNVITA---GPR 28
                                                                                                                                                                            Sequence 4, Application US/08852743
Patent No. 5830699
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09185370 Patent No. 6093560 GENERAL INFORMATION:
  ä
                                         11 AFGAPVWDDNNVITAGPRG 29
                                                                  13 AFGAGTWDKVSVSIVGTRG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-852-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                         US-08-852-743-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-185-370-4
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY:
STATE:
  Matches
                                                                            g
                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                            APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: 0.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 4; Length 209;
Pred. No. 20;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CORRESEDE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPRONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
                                                                                                           US-08-461-002-4; Sequence 4, Application US/08461002; Patent No. 6214543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08689411 Patent No. 6224881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.0
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
; FRAGMENT TYPE: unknown
US-08-461-002-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | |:| || ||
1 VNADIKATTVFG 12
    2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-689-411-4
                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 3; Length 209;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATR:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 manno acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB Pred. No. 4.5; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                    NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/CDCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-464-052-4; Sequence 4, Application US/08464052; Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                Query Match 28.0%;
Best Local Similarity 66.7%;
Matches 8; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 66.7.
انام 8; Conservative
                                                                                                                                                                                                   LENGTH: 60 amino acids TYPE: amino acid
                                                                                                                                                                                                                                       SS: single
unknown
                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-689-411-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide FRAGMENT TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-464-052-4
```

ð g ö

; 0

õ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
US-08-01-71-2
Sequence 2, Application US/08001711
Sequence 2, Application US/08001711
Sequence 2, Application US/08001711
Sequence 3, Application US/08001711
Sequence 4, Application 1548726
Sequence 5, Application 1548726
Sequence 6, JEAN-PIERRE
SEPLICANT: BELLOCQ, JEAN-PIERRE
SEPLICANT: CHAMBON, PIERRE
SEPLICANT: CHAMBON, PIERRE
SEPLICANT: CANCER
SEQUENCE 5, CANCER
SETTLE OF INVENTION: CANCER
SEQUENCE ADDRESS:
SECUENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 488;
Pred. No. 57;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                               Score 44; DB 1; Length 488;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1225 Connecticut Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20036
COMPUTER TO SUITE FLORY:
MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC COMPATIONS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/001,711
FILING DATE: 19930107
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/794,393
FILING DATE: 11-NOV-1991
PRIOR APPLICATION NUMBER: GB 9025626.1
FILING DATE: 21 NOV-1991
PRIOR APPLICATION NUMBER: GB 9025626.1
FILING DATE: AND OFFICE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Suite 300
                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1383.0040001
                                                                                                                                                                                                                                                                                                                                                                                                                                     :| : |:|| | :|
121 LVQEQVRQTMAEALKVWSDVTPLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVNKDVKQTTAFGAPVWDDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVNKDVKQTTAFGAPVWDDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)466-0800
TELEFAX: (202)833-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%;
37.5%;
                                                                                                                                                                                                                                                                   28.0%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                   LENGTH: 488 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-794-393-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 488 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                   Best_Local Similarity 37.59
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.5'
                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-001-711-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 23
S-07-794-393-2
Sequence 2, Application US/07794393
Sequence 2, Application US/07794393
Patent No. 5236844
GENERAL INFORMATION:
APPLICANT: CHAMBON, PIERRE
APPLICANT: BASSET, PAUL
APPLICANT: BELLOCQ, JENN-PIERRE
TITLE OF INVENTION: CANCER
UNDMER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 4; Length 209;
Pred. No. 20;
1; Mismatches 3; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: GOLDman, Michael L.
REGISTRATION NUMBER: 19603/187
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION NIVEORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 aniho acids
TTELEPA: Aniho acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,393
FILING DATE: 19911121
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: GB 9025326.1
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 1383.0040000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.0%;
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || |:| || ||
1 VNADIKATTVFG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-689-411-4
```

ò g ó

```
Sequence 2, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                 OTHER INFORMATION: Description of Unknown Organism: Known Member of
OTHER INFORMATION: Matrix Metalloproteinase Family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 3; Length 511;
Pred. No. 60;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                          Score 44; DB 4; Length 489;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19603/185 (D-1485B)
                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LVQEQVRQTMAEALKVWSDVTPLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: GOLDMAN, MICHAEL L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960:
TELECOMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFRAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVNKDVKQTTAFGAPVWDDNNVIT 24
CURRENT FILING DATE: 1995-06-07
                                                                                                                                                                      OTHER INFORMATION: X = UNKNOWN
                                                                                                                                                                                                                                                                                                                          Query Match 28.0%;
Best Local Similarity 37.5%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.0%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 511 amino acids
amino acid
                    NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                        TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                             US-08-448-489-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-464-052-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-464-052-2
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08448489

Patent No. 6184022

GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SINAGAMA Akira
APPLICANT: SINAGAMA, Akira
APPLICANT: SINAGAMA, Akira
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
                                                      Sequence 22, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILL, Horst
APPLICANT: WILL, Horst
APPLICANT: HINZANN, BEIND
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: LIBM PC COMPATIBLE
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 21-OCT-1994
PRIOR APPLICATION NUMBER: DE 4438838.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, PATLICIA D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 33,683
TRELEPHANE: (202)672-5309
TRELEFAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| : |:|| | :| 11 | 121 LVQEQVRQTMAEALKVWSDVTPLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVNKDVKQTTAFGAPVWDDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                        ZIP: 2007-5109

ZIP: 2007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: LENGTH: 488 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.0%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-08-704-711A-22
                               US-08-704-711A-22
                                                                                                                                                                                                                                                                                                                        STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-448-489-11
```

```
28.0%; Score 44; DB 4; Length 511; 66.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
APPLICANT: CLINTON: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES:
ADDRESSEB: ADDRESS:
ADDRESSEB: ADDRESS:
ADDRESSEB: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 44; DB 5; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
RECISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716,263-1000
TELEPAX: (716,263-1600
TELEPAX: (7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 19603/187
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFEXX: (716) 263-1304
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 511 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Clinton Square
CITY: Rochester
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-689-411-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || |:| || ||
61 VNADIKATTVFG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-09863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-09863-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-689-411-2

Sequence 2, Application US/08689411

Patent No. 6224881

GENERAL INFORMATION:

APPLICANT: Riley M.D., Lee W.

APPLICANT: Chong, Pele

TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES

TITLE OF INVENTION: THERROF

TITLE OF INVENTION: THERROF

CORRESPONDENCES: 14

CORRESPONDENCES: 14
                                                                             Sequence 2, Application US/08461002
Patent No. 6214543
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 4; Length 511;
Pred. No. 60;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
RECISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 511 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VNADIKATIVFG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York COUNTRY: U.S.A. ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Clinton
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                 RESULT 28
US-08-461-002-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-461-002-2
```

õ g

ö

Gaps

ë,

```
Gaps
                                                                                                                                                                                                                                                                                                Score 43.5; DB 3; Length 602;
Pred. No. 88;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Broomlield, Clarence A
APPLICANT: Broomlield, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
CORRESPONDENCE: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43.5; |
Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             broomfield
                                                                                                                                                                                                                                                                                                                                                                                                                 349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                           2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glanna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broom
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-426
INFORMATION: CASE OF THE SECUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.7%;
50.0%;
                                                                                                                                                                                                                                                                                                    Query Match 27.7%;
Best Local Similarity 50.0%;
Matches 14; Conservative
                                                                                                                                                                                                                       ; ORGANISM: human esterases US-08-446-100-1
                  LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: 602 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRACMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: human esteras
                                                                                                                                                   ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
  SEQUENCE CHARACTERISTICS
                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-446-100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-446-100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö,
                      ö
                      Gaps
                                                                                                                                                                                                              Sequence 2, Application US/08907229A

Patent No. 6072048

GENERAL INFORMATION:
TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR UPTAKE OF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
TITLE OF INVENTION: WYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
TITLE OF INVENTION WYGOBACTERIUM TUBERCULOSIS AND USES THEREOF
CURRENT FILING DATE: 1997-08-06
EARLIER APPLICATION NUMBER: 60/040,097
EARLIER FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Broomfield, clarence A
APPLICANT: Milard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTIOR: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.0%; Score 44; DB 3; Length 527; 66.7%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY 1995
CLASSIFICATION: 435
                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
  Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION UNBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-2767
INFORMATION FOR SEQ 1D NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis US-08-907-229-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.0
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |:| || ||
179 VNADIKATTVFG 190
                                                               2 VNKDVKQTTAFG 13
                                                                                      2 VNKDVKQTTAFG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Hend
STREET: 9669 A
CITY: Fairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 527
                                                                                                                                                                                              US-08-907-229-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-446-100-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  á
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
WUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Pairfax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.7%; Score 43.5; D
50.0%; Pred. No. 88;
ive 5; Mismatches
                                                                                                                                                                                                                                                                                  APPLICATION UNMBER: US/08/446,100
CLASSIFICATION 435
CLASSIFICATION 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Droomfield
TELEPHONE: (703) 425-2767
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSS: single
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDALL
STREET: 900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                           ns
                                                                                                 STATE: VA
COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VA
COUNTRY: US
ZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-446-100-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-446-100-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08446100
Patent No. 6001625
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.7%; Score 43.5; D
50.0%; Pred. No. 88;
tive 5; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        broomfield
                                                                349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                         2 VNKDVKQTTAF --- GAPVW -- DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                             US-08-446-100-3; Sequence 3, Application US/08446100; Patent No. 6001625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORREY AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION UNMBER: 32,535
REFERENCE/DOCKET UNMBER: broof
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.09
Matches 14; Conservative
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-446-100-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-446-100-4
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
  Matches
                                                                               q
                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
```

3;

.. M

```
Gaps
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Broomfield, Clarence A
APPLICANT: Milard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREE: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
COUNTY: LOS
ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION NUMBER: US/08/446,100
FILING DATE: Hendricks, Glenna
REGISTRATION NUMBER: 32.35
REFERENCE/DOCKET NUMBER: 32.35
REFERENCE/DOCKET NUMBER: BLOOMfield
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 32.55
TELECOMMUNICATION NUMBER: 32.55
TELECOMMUNICATION NUMBER: 32.576
TELECHONE: (703) 425-2767
INFORMATION FOR SEQ ID NO: 7:
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 602;
                                                                                                                                                          Score 43.5; DB 3; Length 602;
Pred. No. 88;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.7%; Score 43.5; I Best Local Similarity 50.0%; Pred. No. 88; Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                        2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                            US-08-446-100-7; Sequence 7, Application US/08446100; Patent No. 6001625
                                                                                                                                                               27.7%;
50.0%;
                                                                     ORGANISM: human esterases US-08-446-100-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINALY SOURCE:
ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i: 602 amino acids
amino acid
                          N-terminal
                                                                                                                                                            Query Match
Best Local Similarity 50.09
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JACANUEDNESS: single TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHEILCAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-446-100-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Broomfield, Clarence A
APPLICANT: Broomfield, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: broomfield
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.7%; Score 43.5; D
50.0%; Pred. No. 88;
ative 5; Mismatches
                                                                                              broomfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||| : ||| : |:|| 374 | 349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                ATTORREY AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTATION UNDRER: 32,535
REFERENCE/DOCKET NUMBER: Droof
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 425-426
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 maino acids
TYPE: anino acid
TYPE: anino acid
TYPE: anino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            % Sequence 6, Application US/08446100 ; Sequence 6, Application US/08446100 ; Patent No. 6001625 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 22031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-446-100-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

```
Search completed: August 22, 2002, 07:44:34 Job time: 93 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 VNKD--EGTAFLVYGAPGFSKDNNSIIT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-446-100-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-446-100-11
Sequence 11, Application US/08446100
Sequence 11, Application US/08446100
GENERAL INFORMATION:
APPLICANT: Broomfield, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                APPLICANT: Broomfeeld, Clarence A
APPLICANT: Millard, Charles B
APPLICANT: Lockridge, Oksana
TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                             COUNTRY: UDS

ZIP: 22031
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Droomfield
TELEPHONE: (703) 425-4250
TELEPHONE: (703) 425-4250
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENETHOLE CHARACTERISTICS:
                                                                                                                                                                                                                    ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Hendricks and Assoc.
STREET: 9669 A Main Street, P.O. Box 2509
CITY: Fairfax
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.7%; Score 43.5; Dest Local Similarity 50.0%; Pred. No. 88; Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VNKDVKQTTAF---GAPVW--DDNNVIT 24
                  Sequence 8, Application US/08446100 Patent No. 6001625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human esterases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-446-100-8
US-08-446-100-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,100
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REGISTRATION NUMBER: 32,535
REFERENCE/DOCKET NUMBER: 32,535
REFERENCE/DOCKET NUMBER: Droomfield
TELECOMMULCATION INFORMATION:
TELEPHONE: (703) 425-2767
TELEFAX: (703) 425-2767
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.7%; Score 43.5; I Best Local Similarity 50.0%; Pred. No. 88; Matches 14; Conservative 5; Mismatches
```

catalase (EC 1.11.	hypothetical protecatalase (EC 1.11. catalase (EC 1.11. catalase (EC 1.11. catalase (EC 1.11. catalase (EC 1.11. rec7 protein - fis meiotic recombinat catalase (EC 1.11.	catalase (EC 1.11. catalase (EC 1.11. catalase (EC 1.11. chitinase (EC 1.11. catalase vC1585 [1. organic solvent to organic solvent to probable benzoate catalase (EC 1.11. hypothetical prote catalase (EC 1.11. hypothetical prote	catalase (EC 1.11. probable LysR-fami catalase (EC 1.11. protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein T27Al0.6 catalase (EC 1.11. protein glh-1 [imp ATP-dependent RNA F19K19.13 protein origin recognition protein-tyrosine-p pypothetical protein-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p pypothetical protein-p protein-tyrosine-p pypothetical protein-p
64 40.8 492 2 T06478 64 40.8 492 2 S52079 64 40.8 504 2 D81224 64 40.8 504 2 D81224 64 40.8 527 1 CSRT 63 40.1 492 2 S71455 63 40.1 507 2 AD3621 62 39.5 482 2 S49465 63 9.5 705 2 B95843	60 38.2 349 2 C86662 59 37.6 492 2 T12300 59 37.6 492 2 T12300 58 36.9 485 2 709754 57 36.3 249 2 T45217 57 36.3 50 1 CSB0 57 36.3 50 1 CSB0 57 36.3 524 2 T27178 56 35.7 527 2 A36595 56 35.7 527 2 A36595	54 34.4 489 2 A49388 54 34.4 489 2 A49388 54 34.4 535 2 S60265 54 34.4 535 2 S65762 54 34.4 784 1 C64726 54 34.4 784 2 C82183 54 34.4 784 2 C82487 54 34.4 784 2 C85487 55 33.8 169 1 S23478 52 33.1 112 2 T26105 52 33.1 112 2 T26105 53 33.1 488 2 A11796 51 32.5 105 2 A44639	7.3 51 32.5 488 2 A40367 7.4 50 31.8 252 2 C83877 7.5 50 31.8 327 2 E95395 7.6 50 31.8 128 2 537055 7.7 50 31.8 128 2 537055 7.9 49 31.2 456 2 D70772 81.4 8 30.6 474 2 55763 82 48 30.6 604 2 C87818 84 48 30.6 604 2 T59132 85 48 30.6 604 2 T59132 86 48 30.6 604 2 T59132 87 48 30.6 604 2 T6913 88 48 30.6 1226 2 J5970 89 48 30.6 1297 2 T39287 91 47 29.9 187 2 T39287 92 47 29.9 187 2 T39287 93 47 29.9 187 2 H34698 94 47 29.9 617 2 E64734 95 47 29.9 617 2 E64734 96 47 29.9 187 2 T34290 97 47 29.9 617 2 E64734 98 47 29.9 759 2 T42027
	1 4 4 4 4 4 4 4 4 4 4 M I I I I I I I I I		
version 4.5 - 2000 Compugen Ltd. model 46:12; Search time 26.88 Seconds (without alignments) 103.668 willion cell undates/sec	29 s: 283138	results predicted by chance to have a lot the score of the result being printed, of the total score distribution. SUMMARIES ID	catalase (EC 1.11.
GenCore versi Copyright (c) 1993 - 200 OM protein - protein search, using sw mode Run on: August 22, 2002, 07:46:12	8-737-2 KQTTAFGAPVWDDN .0 , Gapext 0. eqs, 96089334 sfying chosen 000000000	first 11 * * mber of or equanalysis gth DB	1 157 100.0 505 2 C64629 3 93 59.2 484 2 A58663 4 88 56.1 480 2 A50157 5 83.5 53.2 491 1 CSR2 7 8 5 53.2 494 2 S62697 7 8 49.7 482 2 B83113 10 76 484 4 492 2 B1313 11 75 47.8 49.7 2 B83113 12 75 47.8 49.2 2 B83113 14 47.1 507 2 G89908 15 73 46.5 480 2 JC7679 17 45.9 493 2 T10902 18 71 45.9 493 2 T10902 19 70 44.6 492 2 S1043 10 70 44.6 492 2 S10791 10 70 44.6 493 2 JC7679 11 72 45.9 493 2 T10902 12 75 483 2 A65297 13 46.5 483 2 JC6791 14 6 492 2 T10902 15 73 46.5 483 2 JC7691 16 43.3 492 2 S17493 24 65 43.3 492 2 S17493 25 66 42.0 527 1 CSY 26 66 42.0 527 2 CSFW 27 42.7 492 1 CSY 28 65 41.4 486 2 A57262

08:03:51

22

Thu Aug

```
C; Accession: A58663; B58663
R; Buzy, A.; Bracchi, V.; Sterjiades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jo J. Protein Chem. 14, 59-72, 1936
A; Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of A; Reference number: A58663; MUID:95305957
A; Reference number: A58663; MUID:95305957
A; Accession: A58663
A; Molecule type: protein
A; Residues: 1-484 <BUZI>A; Accession: B58663
A; Molecule type: DNA
A; Residues: 1-305, AE' CBUZZ>A; Molecule type: DNA
A; Reference number: A67999; PDB:2CAE
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Contents: Annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S60757
R; DeShazer, D.; Wood, G.E.; Friedman, R.L.
Mol. Microbiol. 14, 132-130, 1994
A; Title: Molecular characterization of catalase from Bordetella pertussis: identifica A; Reference number: S60757; MUID: 95131725
A; Accession: S60757
A; Molecular preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-482 <DSS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: Chromoprotein; heme; homotetramer; iron; metalloprotein; NADP; oxidoreduc F;53,Modified site: methionine sulfone (Met) #status experimental F;54,93,127/Active site: His, Ser, Asn #status predicted F;34,93,127/Active site: His, Ser, Asn #status predicted F;33/Asinding site: heme iron (Tyr) (axial ligand) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: catalyzes the conversion of two of molecules of hydrogen peroxide to A; Note: this enzyme has a tightly bound NADPH cofactor C; Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475 A;Note: native Fe(III) with NADPH R;Gouet, P.; Jouve, H.M.; Dideberg, O. J. Mol. Biol. 249, 933-94, 1995 A;Title: Crystal structure of Proteus mirabilis PR catalase with and without bound A;Feference number: A58664; MUID:95311317 A;Contents: annotation; X-ray crystallography, 2.2 angstroms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signote, P.; Jouve, H.M.; Hajdu, J.
submitted to the Brookhaven Protein Data Bank, June 1996
A; Reference number: A67901; PDB:2CAG
A; Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
A; Note: compound II, dithiothreitol reduced compound I
R; Goulet, P.; Jouve, H.M.; Dideberg, O.
submitted to the Brookhaven Protein Data Bank, July 1996
A; Reference number: A67902; PDB:2CAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            catalase (EC 1.11.1.6) - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 27-Apr_1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
                                                                                              A, Variety: strain Pr, peroxide resistant
C;Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
catalase (EC 1.11.1.6) [validated] - Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 2; Pred. No. 7.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.2%;
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                 C; Species: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Complex: homotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S60757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catalase (EC 1.11.1.6) - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C;Accession: F71885
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
I Jves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71805
A;Accession: F71885
A;Accession: F71885
A;Molecule type: DNA
A;Residues: 1-505 caRN>
A;Molecule type: DNA
A;Residues: 1-505 caRN>
A;Cross-references: GB:AE001510; GB:AE001439; NID:94155371; PIDN:AAD06391.1; PID:9415538
A;Genetics:

                                                                                                                                                                                                                                                                                                                                                                 C; Accession: G64629
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Reterson, J.E.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A; Reference number: A64520; MUID:97394467
A; Reference number: A64520; MUID:97394467
A; Residues: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-505 < CMA>
A; Residues: 1-505 < CMA>
A; Coss-references: GB:AE000597; GB:AE000511; NID:g2314007; PIDN:AAD07923.1; PID:g231401
C; Superfamily: catalase
C; Reywords: chromoprotein, heme; 1ron; metalloprotein; oxidoreductase
F; 56, 95, 129/Active site: His, Ser, Asn #stetus predicted
F; 359/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                           Species: Helicobacter pylori
Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 157; DB 2; Length 505; 100.0%; Pred. No. 2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                         catalase (EC 1.11.1.6) - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 157; DB 2, ilarity 100.0%; Pred. No. 2e-15; Conservative 0; Mismatches '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
A58663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

ò

ò

ΝĀ

ij

```
Catalase (EC 1.11.1.6) 3 - maize
Cispecies: Zea mays (maize)
Cispecies: Zea mays (maize)
Cispecies: Zea mays (maize)
Cispecies: 2.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 04-Mar-2000
Cispaces: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 04-Mar-2000
Cispaces: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 04-Mar-2000
Cispaces: 31-Dec-1993 #sequence of a genomic sequence encoding the maize Cat3 A; Title: Isolation and characterization of a genomic sequence encoding the maize Cat3 A; Reference number: S37379; MUID:94003062
A; Accession: S37379
A; Molecule type: DNA
A; Residues: 1-496 <ABL>
A; Coss - references: GB:L05934; NID:9168436; PIDN:AAC37357.1; PID:9168437
A; Experimental source: variety L W64A
A; Residuabugh, M.G.; Wadsworth, G.J.; Scandalios, J.G.
Biochim: Biophys. Acta 951, 104-116, 1988
A; Felerence number: JA0091; MUID:89051000
A; Residues: 1-56.D', S8-78, S', 80-106, 'Q', 108-109, 'P', 111,'P', 113-114,'GR', 117-120,'A
A; Molecule type: mRNA
A; Residues: 1-56.D', S8-78, 'S', 80-106, 'Q', 108-109, 'P', 111,'P', 113-114,'GR', 117-120,'A
A; Note: the authors translated the codon GAG for residue 234 as Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Hordeum vulgare (barley)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
C;Accession: S62697
R;Skadsen, R.W.; Schulze-Lefert, P.; Herbst, J.M.
Plant Mol. Biol. 29, 1005-1014, 1995
A;Title: Molecular cloning, characterization and expression analysis of two catalase A;Reference number: S62696; MUID:96145511
A;Accession: S62697
A;Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
A;Cross-references: EMBL:X61626; NID:g20191; PIDN:CAA43814.1; PID:g20192 C;Genetics:
A;Gene: cat A
A;Introns: 5/3; 272/3; 472/3
C;Superfamily: catalase
C;Superfamily: catalase
C;Superfamily: catalase
F;65.104,138/Active site: His, Ser, Asn #status predicted
F;55.104,138/Active site: His, Ser, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: chromoprotein; heme; iron; metalloprotein; mitochondrion; F; 67, 106, 140/Active site: His, Ser, Asn #status predicted F; 351/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 2; Len
Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                           Score 83.5; DB 1;
Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalase (EC 1.11.1.6) isoenzyme 2 - barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 53.2%;
Best Local Similarity 61.5%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 52.2%;
Best Local Similarity 66.7%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 TINAGAPVWNDNEALTVGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 7/3; 477/3
C; Superfamily: catala:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: cat3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Accession: $70588
A. Status: preliminary
A. Molecule type: DNA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Oryza sativa (rice)
C; Date: 31-Dec-1992 #sequence_revision 02-Jun-2000 #text_change 16-Jun-2000
C; Accession: 870588; S20873; S19823
R; Higo, K.; Higo, H.
Biol. 30, 505-521, 1996
A; Title: Cloning and characterization of the rice CatA catalase gene, a homologue of the A; Reference number: 870588; MUID:96189265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R. Parkhill, J.: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A. Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A. Reference number: AB0001; MUID:21470413; PMID:11586360
A;Cross-references: EMBL:U07800; NID:g494943; PIDN:AAA18481.1; PID:g494944 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AL590842; PIDN: CAC90045.1; PID: 915979266; GSPDB: GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catalase (EC 1.11.1.6) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                  C; Superfamily: catalase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;57,96,130/Active site: His, Ser, Asn #status predicted
F;340/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DD ...
. 7.9e-05;
...a 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB 2; Length 480;
Pred. No. 7.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                           Length 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-112, 'Q', 114-447, 'AV', 450-491 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MTNKTL--TTAAGAPVADNNNTMTAGPRG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalase (EC 1.11.1.6) catA - rice
                                                                                                                                                                                                                                                                                                                                                                                           56.1%;
d5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%;
65.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: katA
C,Superfamily: catalase
C,Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: AB0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                      A; Gene: catA
                                                                               Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

oxidoreductase;

οy g

```
Actions (EC 1.11.1.6) - Arabidopsis thaliana
NyAlternate names: protein M4E13.140
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
Cisacession: T05779; S18972
Cisacession: T05779; S18972
A:Reference number: 215451
A:Reference number: 215451
A:Residues: 1-492 ABP>
A:Residues: 1-492 ABP>
A:Cross-references: EMBL:AL022023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Experimental source: cultivar Columbia; BAC clone M4E13
R;Chevalier, C; Yamaguchi, J; McCourt, P.
submitted to the EMBL Data Library, January 1992
A;Description: Isolation and characterization of a catalase cDNA from Arabidopsis tha A;Reference number: $18972
                                                                                                                                                                                                                     catalase (EC 1.11.1.6) - upland cotton
C:Species: Gossypium hirstuum (upland cotton)
C:Species: Gossypium hirstuum (upland cotton)
C:Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 04-Mar-2000
C;Accession: S10770
R:Mi, W.; Turley, R.B.; Trelease, R.N.
Biochim. Biophys. Acta 1049, 219-222, 1990
A;Title: Characterization of a cDNA encoding cottonseed catalase.
A;Accession: S10770
A;Residues: 10770; MUID:90304227
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-492 <NIW>A;Residues: 1-492 <NIW>A;Cross-references: GB:X52135; NID:g18483; PIDN:CAA36380.1; PID:g18484
C:Superfamily: catalase
C;Superfamily: catalase
C;Superfamily: atalase
C;Superfamily: Ashative site: His, Ser, Ash #status predicted
F;55,104.138/Active site: His, Ser, Ash #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; MOlecule type: mRNA
A; Residues: 1-38,'L',40-108,'A',110-153,'I',155-242,'L',244-492 <CHE>
A; Cross-references: EMBL:X64271; NID:g16214; PIDN:CAA45564.1; PID:g16215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: catalase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 4
A; Introns: 5/3; 38/1; 130/3; 389/3; 419/3; 442/2; 473/3
A; Note: M4E13.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.4%; Score 76; DB 2;
61.9%; Pred. No. 0.0025;
tive 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.8%; Score 75; DB 2; llarity 61.9%; Pred. No. 0.0036; Conservative 4; Mismatches 4
                                   29
                                                                18 TINSGAPVWNNNSSLTVGPRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S18972
                                                                                                                                                                         11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathq A.Accession: B83113
A.Accession: B83113
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-482 <STO>
A;Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: BB3113
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larb Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase (EC 1.11.1.6) chain 1 - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Mar-2000
C;Accession: S10395
R;Weiting, N.; Turley, R.B.; Trelease, R.N.
submitted to the EMBL Data Library, March 1990
A; Molecule type: mRNA
A; Residues: 1-494 <SKA>
A; Cross-references: EMBL:U20778; NID:g684947; PIDN:AAA96948.1; PID:g684948
A; Orose: the authors did not translate the codon for residue 76
C; Superfamily: catalase
C; Seperfamily: catalase
C; Keywords: heme; iron; metalloprotein; oxidoreductase
F; 65, 104, 138/Active site: His, Ser, Asn #status predicted
F; 55, 104, 138/Active site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Rolecule type: mRNA
A.Residues: 1-492 <WEI>
A.Cross-references: EMBL:X52135
C.Superfamily: catalase
C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                         Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 2; Length 492
Pred. No. 0.0025;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB ... 0.0012;
                                                                                                                                                                                                                                                                                   Score 78.5; DB 2;
Pred. No. 0.0011;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                            5 DVKQTTA-FGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: strain PAO1 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 61.9%;
Matches 13; Conservative 4
                                                                                                                                                                                                                                                                                Query Match 50.0%;
Best Local Similarity 57.7%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 49.7%;
1 Similarity 57.1%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S10395
A; Accession: S10395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: katA; PA4236
C;Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
```

ò q

ö

```
C; Accession: JC7672
B; Kitamura, M.; Nakanishi, T.; Kojima, S.; Kumagai, I.; Inoue, H.
J. Biochem. 129, 357-364, 2001
J. Biochem. 129, 357-364, 2001
J. Biochem. 129, 357-364, 2001
J. Fitle: Cloning and expression of the catalase gene from the anaerobic bacterium Des A; Reference number: JC7672; MUID:21125589; PMID:11226874
A; Reference number: JC7672; MUID:21125589; PMID:11226874
A; Residues: JC480
A; Residues: 1-480 < KIT>
A; Residues: 1-480 < KIT>
A; Comment: This enzyme, one of the hemoproteins, located in the cytoplasm, functions C; Genetics:
C; Comment: This enzyme, one of the hemoproteins, located in the cytoplasm, functions C; Genetics: kat
A; Gene: kat
C; Superfamily: catalase
C; Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t
W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF016902; NID:g2388690; PIDN:AAB70006.1; PID:g2388691
A;Experimental source: strain CC-125 wild type mt+ 137c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catalase (EC 1.11.1.6) - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Vigna radiata (mung bean)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.5%; Score 73; DB 2; Length 492; 61.9%; Pred. No. 0.0071;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 2;
Pred. No. 0.0069;
2; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T07911; T08127
R;Kim, J.Y.; Lee, K.O.; Lee, S.H.
Submitted to the EMBL Data Library, August 1997
A;Reference number: Z16209
A;Accession: T07911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalase (EC 1.11.1.6) - mung bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.5%;
ilarity 65.2%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-493 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                        catalase (EC 1.11.1.6) isoenzyme 1 - barley
Cispecies: Hordeum vulgare (barley)
Cispecies: Societare (barley)
Cispecies: Nob. 1997
Cispecies: Nob. 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catalase [imported] - Staphylococcus aureus (strain N315)
Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cispecies: 00-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Cishcossion: G89908
Cishiba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, L.; Cishiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Cishiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
AiTitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
AiReference number: A89758; MuID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-507 <KUR>
A;Cross-references: GB:BAQ00018; PID:g13701132; PIDN:BAB42427.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: kath
C;Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JC7672
catalase (EC 1.11.1.6) - Desulfovibrio vulgaris
C;Species: Desulfovibrio vulgaris
C;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 492,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74; DB 2;
Pred. No. 0.005;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 MSQQDKKLTGVFGHPVSDRENSMTAGPRG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 TINSGAPVWNNNALTVGHRG 38
                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 47.1%;
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.18;
55.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 47.1
Best Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
G89908
                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                ô
                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

ø

ဌ

```
RESULT 19
State (EC 1.11.1.6) 1 - maize
Catalase (EC 1.11.1.6) 1 - maize
Catalase (EC 1.11.1.6) 1 - maize
C; Species: Zea mays (maize)
C; Date: 14-u1-1995 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
R; Guan, L.; Scandalios, J.G.
Phant J. 3, 527-536, 1993
A; Title: Characterization of the catalase antioxidant defense gene Catl of maize, and A; Reference number: S48124, MUID:94035156
A; Molecule type: DNA
A; Residues: 1-492 <GUA>
A; Cross-references: EMBL: X60135; NID:9311238; PIDN:CAA42720.1; PID:9311239
A; Title: Characterization of catalase transcripts and their differential expression i A; Reference number: JA0090; MUID:89051000
A; Molecule type: mRNA
A; Residues: 1-156, 'A, '158-210, 'S, '212-328, 'S', 330-482,'P', 484-492 <RED>
A; Cross-references: GB:X12538; GB:M33104; NID:922231; PIDN:CAA31056.1; PID:922232
A; Cross-references: GB:X12538; GB:M33104; NID:922231; PIDN:CAA304010405
A; Dromoprotein; heme: iron; metalloprotein; oxidoreductase
C; Keywords: chromoprotein; heme: iron; metalloprotein; oxidoreductase
F; 65, 104, 138/Active site: His, Ser, Asn #status predicted
F; 55, 104, 138/Active site: His, Ser, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: Agrobacterium tumefaciens (strain C58, Dupont) plasmid AT C; Species: Agrobacterium tumefaciens C; Accession: AC3220 C; Accession: AC3220 C; Accession: AC3220 C; Accession: AC3220 C; Guenthner, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wood, D; Karb, D.; Romero, P.; Zhang, S. Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl A; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam Ster, E.W. A; Telefrence number: AB2577; PMID:11743193 A; Accession: AC3220
catalyzes the conversion of two of molecules of hydrogen peroxide
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
A; Description: catalyzes the conversion of two of molecules of hydroge C; Superfamily: catalase
C; Seywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F; 2-483/Product: catalase, vegetative #status predicted <MAT>
F; 54,93,127/Active site: His, Ser, Asn #status predicted
F; 337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                        Score 71; DB 2; Length 483;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.6%; Score 70; DB 2; Length 492; 57.1%; Pred. No. 0.02; tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                    45.2%; bcc. 60.9%; Pred. No. c..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || |||||::|: :| | || || TINSGAPVWNNNSALTVGQRG
                                                                                                                                                                                                                                                                                                            Query Match 45.2
Best Local Similarity 60.9
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Rolecule type: DNA
A; Residues: 1-483 < Poly.
A; Rolecule type: DNA
A; Residues: 1-483 < Poly.
A; Cross-references: GB: M80796; NID:g142860; PIDN: AAA22402.1; PID:g142861
B; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter
B; Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; Chd
A; Ehrlich, S:D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y; Funa, S; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, R.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tergstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, R.
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Tele: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Accession: C65647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
C;Accession: J40532; C69647; F44519
R;Bol, D.K.; Yaabin, R.E.
Gene 109, 31-37, 1991
A;Title: The isoclation, cloning and identification of a vegetative catalase gene from Ba
A;Reference number: J40532; MUID:92097949
                                                                                                                                                                                                                                                                                                                                                                                                                                     mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:Z99108; GB:AL009126; NID:92633055; PIDN:CAB12710.1; PID:92633205
A;Experimental source: strain 168
R;Dowds, B.C.A.
                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-90, 'P',92-244, 'RS',247-356,'V',358-404,'GWLPCRV',413-434,'RW',437-481,'G'
A; Cross-references: EMBL:Y13220
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: catalyzes the conversion of two molecules of hydrogenperoxide to two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: catalase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Dowds, B.C.A.
submitted to the Protein Sequence Database, February 1993
A;Reference number: A44519
A;Accession: F44519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase (EC 1.11.1.6), vegetative - Bacillus subtilis N;Alternate names: catalase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 2;
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-205,'G',207-372,'G',374-483 <KUN>
                                        submitted to the EMBL Data Library, May 1997
                                                                                                                                                A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TINSGAPVWNNNSMTVGTRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 61.99
Matches 13; Conservative
                                                                        A; Reference number: Z16371
A; Accession: T08127
    R; Thome, H.; Happe, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: katA
C;Function:
                                                                                                                                                                                                                                                                                                                                                A; Gene: CAT
C; Function:
                                                                                                                                                                                                                                                                                                                C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ţ

```
catalase (EC 1.11.1.6) 3 - curled-leaved tobacco C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco) C;Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 C;Accession: T16969 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 R;Willakens, H.; Villarroel, R.; van Montagu, M.; Inze, D.; van Camp, W. RFBS Lett. 352, 79-83, 1994 A;Fitle: Molecular identification of catalases from Nicotiana plumbaginifolia (L.).
                                                                                                                                                                  Catalase (EC 1.11.1.6) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 03-Mar-2000
C;Accession: S18346; S1559
R;Isin, S.H; Allen, R.D.
Pant Mol. Biol. 17, 1263-1265, 1991
A;Title: Isolation and characterization of a pea catalase cDNA.
A;Reference number: S18346
A;Reference number: S18346
A;Redicules: 1-494 <ISI.
A;Cross-references: EMBL:X60169; NID:g20676; PIDN:CAA42736.1; PID:g20677
C;Superfamily: catalase
C;Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; peroxisome;
F;65,104,138/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catalase (EC 1.11.1.6) - soybean
C.Species: Glycine max (soybean)
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Mar-2000
C.Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Mar-2000
C.Accession: $20999
R.Allen, R.
submitted to the EMBL Data Library, May 1992
A.Recession: $20999
A.Recession: $20999
A.Molecule type: DNA
A.Residues: 1492 ALL>
A.Cross.references: EMBL: 212021; NID: 918559; PIDN: CAA78056.1; PID: 918560
C.Genetics: A.Introns: 5/3: 38/1; 389/3; 419/3; 442/2; 473/3
C.Genetics: Catalase
C.Genetics: Catalase
C.Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase
C.Keywords: Chromoprotein; heme; iron; metalloprotein; status predicted
F; 55, 104, 138/Active site: His, Ser, Asn #status predicted
F; 348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 42.7%; Score 67; DB 1; Length 492; Best Local Similarity 52.4%; Pred. No. 0.056; Matches 11; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.3%; Score 68; 57.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 TINSGAPIWNNSSLTVGSRG 38
                           18 TTNSGAPVWNNNSSLTVGSRG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 TINSGAPVWNNNSSLIVGSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T16969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
  à
                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                           ö
                                                                      A;Cross-references: GB:AE008687; PIDN:AAL46177.1; PID:g17743948; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalase (EC 1.11.1.6) - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Species: Gossypium hirsutum (upland cotton)
C;Aate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C;Accession: S1493
R;Ni, W.; Trelease, R.N.
Arch. Biochem. Biophys. 289, 237-243, 1991
A;Title: Two genes encode the two subunits of cottonseed catalase.
A;Reference number: S17493; MUID:91378551
A;Accession: S17493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: mRNA
A;Residues: 1-492 <NIW>
A;Cross-references: EMBL:X56675; NID:g18487; PIDN:CAA39998.1; PID:g18488
C;Superfamily: catalases
C;Superfamily: catalase
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;65,104,138/Active site: H1s, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GB:D21161, NID:9532341, PIDN:BAA04697.1; PID:9643601 C.Superfamily: catalase C.Seywords: chromoprotein, heme; iron; metalloprotein; oxidoreductase F:65.104,138/Active site: His, Ser, Asn #status predicted F:348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                        Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.3%; Score 68; DB 2; Best Local Similarity 57.1%; Pred. No. 0.04; Matches 12; Conservative 4; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.3%; Score 68; DB 2; 57.1%; Pred. No. 0.04; vative 4; Mismatches
                                                                                                                                                                                                                                                        Score 69; DB 2;
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                          40 TTAQGAPVADDQNSLRIGPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 TTNSGAPVWNNNSSLTVGARG 38
                                                                                                                                                                                                                                                                                                                                                         9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                        43.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 43.3
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-492 <SUZ>
                  A; Molecule type: DNA
A; Residues: 1-713 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
A;Status: preliminary
                                                                                                                                               A;Gene: catE
A;Genome: plasmid
                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
```

u

```
RESULT 27
S65793
catalase (EC 1.11.1.6) - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 06-Jun-1997
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 06-Jun-1997
C;Accession: S65793
R;Yuan, H.T; Bingle, C.D; Kelly, F.J.
Biochim. Biophys. Acta 1305, 163-171, 1996
A;Title: Differential patterns of antioxidant enzyme mRNA expression in guinea pig lu A;Reference number: S65793; MUID:96180320
A;Accession: S65793
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <YUA>
A;Cross-references: EMML:U39841
C;Superfamily: catalase
C;Keywords: chromoprotein; heme; iron; oxidoreductase
                                                                                   A.Gene: GDB:CAT
A.Cross-references: GDB:119049; OMIM:115500
A.Gene: GDB:CAT
A.Cross-references: GDB:119049; OMIM:115500
A.Map position: 11p13-11p13
A.Introns: 22/3; 80/1; 117/1; 160/3; 195/3; 237/3; 301/3; 352/3; 399/1; 442/3; 478/3;
C.Complex: homotetramer
C.Superlex: homotetramer
A.Description: catalyzes the conversion of two of molecules of hydrogen peroxide to t
C.Superfamily: catalase
C.Keywords: blocked amino end; chromoprotein; heme; homotetramer; iron; metalloprotein
F; 2-513/Product: catalase #status experimental -kMAT>
F; 2-513/Product: catalase, peroxisomal form #status predicted <AMAT2>
F; 217-519/Region: peroxisome/glyoxysome location signal (5-[RKH]-L) motif
F; 2-514/A.L48/Active site: His, Ser. Asn #status predicted
F; 358/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a catalase from the anaerobic bacterium
         C:Comment: Catalase occurs in almost all aerobically respiring organisms and serves C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catalase (EC 1.11.1.6) - Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Accession: A57262
R;Rocha, E.R.; Smith, C.J.
J, Bacteriol. 177, 311-3119, 1995
A;Ritle: Blochemical and genetic analyses of a catalase from the anaerobic k A;Reference number: A57262; MUID:95286491
A;Accession: A57262
A;Status: preliminary
A;Molecule type: DAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-486 <ROC>
A; Cross-references: GB:U18676; NID:g841191; PIDN:AAC43384.1; PID:g841192
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 42.0%; Score 66; DB 1; Best Local Similarity 66.7%; Pred. No. 0.086; Matches 14; Conservative 0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 2
Pred. No. 0.022
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 TTGAGNPVGDKLNVITVGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.4%;
Best Local Similarity 61.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| | || | |::| ||||
TTAGGNPVGDKLNIMTVGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                    A; Accession: T16969
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-492 GMIL>
A; Cross-references: EMBL:236977; NID:9536786; PIDN:CAA85426.1; PID:9536787
A; Experimental source: flower
C; Experimental source: flower
C; Enction:
A; Gene: cat3
C; Function:
A; Description: catalyzes the conversion of two molecules of hydrogenperoxide to two mole
C; Superfamily: catalase
C; Superfamily: (axial iliquid) #status predicted
F; 55,104,138/Active site: His, Ser, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross_references: GB:X04076; NID:g29720; PIDN:CAA27717.1; PID:g29721
B;Korneluk, R.G.; Quan, F.; Lewis, W.H.; Guise, K.S.; Willard, H.F.; Holmes, M.T.; Grave
B;Korneluk, R.G.; Quan, F.; Lewis, W.H.; Guise, K.S.; Willard, H.F.; Holmes, M.T.; Grave
B;Title: Isolation of human fibroblast catalase cDNA clones. Sequence of clones derived
A;Title: Isolation of human fibroblast catalase cDNA clones. Sequence of clones derived
A;Reference number: A00501; MUID:85034813
A;Recession: A00501
A;Molecule type: mRNA
A;Residues: 77-527 < COR>
A;Cross-references: GB:K02400; NID:g940256; PIDN:AAB59522.1; PID:g179950
A;Cross-references: GB:K02400; NID:g940256; PIDN:AAB59522.1; PID:g179950
A;Cross-references: fibroblast
A;Residues: 77-527 < CORS-
A;Cross-references: fibroblast
A;Clin: Invest: 93, 297-302, 1994
A;Title: Vulnerability of the human airway epithelium to hyperoxia. Constitutive express
A;Accession: 155606; MUID:94110338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٦
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:L13609; NID:9388711; PIDN:AAA16651.1; PID:9388712
R; Schroeder, W.A.; Shelton, J.R.; Shelton, J.B.; Apell, G.; Evans, L.; Bonaventura, Arch. Biochem. Biophys. 214, 422-424, 1982
Arch. Biochem. Biophys. 214, 622-424, 1982
A; Title: The partial amino acid sequence of human erythrocyte catalase.
A; Reference number: A44711; MUID:82205136
A; Contents: annotation; sequence of peptides differing in composition from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catalase (EC 1.11.1.6) precursor [validated] - human NiAlternate names: hydrogen peroxidase; hydrogen peroxidase; c.species: Homo sapiens (man) (c.species: Homo sapiens (man) (c.species: Homo sapiens (man) (c.species: I7-Mar-1987 #sequence_revision 18-Aug-1995 #text_change 08-Dec-2000 (c.specession: A23646; A23651; A00501; I55606 (c.specession: A23646; A23651; A00501; I55606 (c.specession: A23646; MUSL) (species) (man) (ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-527 < QQA>
A; Cross-references: GB: XX04085; NID: 929682; PIDN: CAA27721.1; PID: 91228085
A; Cross-references: GB: XX04085; NID: 929682; PIDN: CAA27721.1; PID: 91228085
B; Bell, G.I.; Najarian, R.C.; Mullenbach, G.T.; Hallewell, R.A.
A; Bell, G.I.; Najarian, FS61-5562, 1986
A; Title: CDNA sequence coding for human kidney catalase.
A; Reference number: A23651; MUID: 86286565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 2;
Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
A; Reference number: S48650; MUID:95010681
A; Accession: T16969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.78;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.7
Best Local Similarity 57.1
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-527 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-22 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A23651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Cyacossion: S50079

R;Kleff, S.; Trelease, R.N.; Eising, R.
Biochim. Biophys. Acta 1224, 463-466, 1994

A;Title: Nucleotide and deduced amino acid sequence of a putative higher molecular we A;Reference number: S52079; MUID:95101741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catalase (EC 1.11.1.6) NWA0050 [similarity] – Neisseria meningitidis (strain MC58 ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C. Accession: T12304.

R. Michalowski, C.B.; Quigley-Landreau, F.; Bohnert, H.J.

Submitted to the EMBL Data Library, June 1998

A. Description: Different isoforms of catalase are expressed in leaves and roots of the EMBL Data Library, June 1998

A. Reference number: 217487

A. Accession: T12304

A. Sective: preliminary; translated from GB/EMBL/DDBJ

A. Molecule type: mRNA

A. Residues: 1-493 < MIC>
A. Cross references: EMBL: AF069320; NID: g3202033; PID: g3202034

C. Superfamily: catalase

C. Keywords: heme: iron: metalloprotein; oxidoreductase

F: 55,104,138/Active site: His, Ser, Asn #status predicted

F: 549/Blnding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase (EC 1.11.1.6), root - common ice plant
C;Species: Mesembryanthemum crystallinum (common ice plant)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                      catalase (EC 1.11.1.6) - common sunflower
C;Species: Helianthus annuus (common sunflower)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: mRNA
A; Residues: 1-492 < KLLE>
A; Cross-references: EMBL:L28740; NID:q453528; PIDN:AAA69866.1; PID:q453529
A; Note: the authors translated the codon TTC for residue 103 as Leu
C; Superfamily: catalase
C; Superfamily: catalase
C; Stywords: heme: iron; metalloprotein; oxidoreductase
F; 55.104,138/Active site: His, Ser, Asn #status predicted
F; 55.104,138/Active site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%; Score 64; DB 2; 52.4%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11arity 57.1%; Pred. No. 0.16; Conservative 4; Mismatches
                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
     Š.
     Pred.
                          5;
                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
                                                                                                                           38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Neisseria meningitidis
Similarity 52.4%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 TINSGAPVYNNNSLTVGSRG
                                                                                                                           18 STNSGAPVWNNDNSLTVGSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TTKTGQPVWNDDSSLTVGARG
                                                                             9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 12
     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                         31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33
  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D8122
                                                                             à
                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Molecule type: DID:g1573949; The C:Comment: This predicted catalase is unusual in having Thr-102 replace the catalyticall C:Superfamily: datalase
C:Superfamily: datalase
C:Molecule type: DID:g1573949; The Catalyticall C:Molecule type: DID:g1573949; The C:Comment: This predicted
B:G1.102,136/Active site: His, Thr, Asn #status predicted
F:346/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: D64103
R;FletSchmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: D64103
                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                               catalase (EC 1.11.1.6) - Haemophilus influenzae (strain Rd KW20)
C;Species: Hemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 04-Mar-2000
C;Accession: D64103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Triticum aestivum (common wheat)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06478
R;Saruyama, H.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                  C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;54,93,127/Active site: His, Ser, Asn #status predicted F;337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;65,104,138/Active site: His, Ser, Asn #status predicted F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
                                                                                                                                                      Length 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 508,
                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                   DB 2;
0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 2;
Pred. No. 0.12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substituted to the EMBL Data Library, July 1996
A; Reference number: 215707
A; Accession: T06478
A; Molecule type: mRNA
A; Residues: 1-492 - SARA
A; Cass-references: EMBL: D86327; PIDN: BAA13068.1
A; Experimental source: seedling
                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                   Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%; Score 64;
                                                                                                                                                                                                                                                                                      1 MVNKDVKQTTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.48;
61.98;
                                                                                                                                                   41.4%;
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.9*
Local 13; Conservative
                                                                                                                                                   Ouery Match
Best Local Similarity 55.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalase (EC 1.11.1.6) - wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: catl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

ť

us-09-488-737-2.rpr

ö

```
Schooles: Zea mays (maize)
C;Species: Zea mays (zea maize)
Z;Schooles: Zea mays (zea maize)
R;Guan, L.; Polidoros, A.N.; Scandalios, J.G.
R;Guan, L.; Ruzas: S71455
R;Status: S71455
R;Status: Sreliminary
R;Molecule type: DNA
A;Residues: 1-492 cGUA>
A;Residues: 1-492 cGUA>
A;Residues: 1-492 cGUA>
A;Residues: La maiditional T the nucleic acid sequence submitted to the EMBL Data L
A;Note: the authors translated the codon AAC for residue 28 as Met, GCC for residue 2
R;Guan, L.; Ruzas, S.; Skadsen, R.W.; Scandalios, J.G.
R;Guan, L.; Ruzas, S.; Skadsen, R.W.; Scandalios, J.G.
R;Title: Comparison of the cat2 complementary DNA sequences of a normal catalase acti
                                A; Residues: 399-433,'N', 435-527 <RES>
A; Cross-references: GB:K01929; NID:g203346; PIDN:AAA40885.1; PID:g203347
C; Genetics:
A; Gene: cat
A; Introns: 22/3; 80/1; 117/1; 160/3; 195/3; 237/3; 301/3; 352/3; 399/1; 442/3; 478/3;
C; Complex: homotetramer
                                                                                                                                                                                                                                                                                            A) Description: catalyzes the conversion of two of molecules of hydrogen peroxide to C; Superfamily: catalase C; Separamer; iron; metalloprotein; oxidoreductase; C; Kaybords: chromoprotein; heme; homotetramer; iron; metalloprotein; oxidoreductase; E; 75, 114, 148/Active site: His, Ser, Asn #status predicted F; 358/Blinding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-240, "RC', 244-296, 'T', 298-492 <GUW>
A; Cross-references: EMBL:X54819; NID:g22233; PIDN:CAA38588.1; PID:g22234
A; Cross-references: EMBL:X54819; NID:g22233; PIDN:CAA38588.1; PID:g22234
B; Rethards, L.A.; Skadsen, R.W.; Scandalios, J.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6927, 1990
A; Reference number: A36062; MUID:90370897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Superfamily: catalase
C.Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;64,103,137/Active site: His, Ser, Asn #status predicted
F;348/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J02976
A;Note: the authors translated the codon AAC for residue 124 as Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.1%; Score 63; DB 2; Length 492; 52.4%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-123,'N',125-240,'RC',244-296,'R',298-492 <BET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 1;
Pred. No. 0.17;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 5/3; 38/1; 419/3; 442/2; 473/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 TTGGGNPIGDKLNIMTAGPRG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.8%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-123,'N'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S18819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: erratum
A; Accession: A36062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                   C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule from:
A:Residues: 1-504 cTET>
A:Cross-references: GB:AE002379; GB:AE002098; NID:g7225435; PIDN:AAF40672.1; PID:g722543
A:Cross-references: GB:AE002379; GB:AE002098; NID:g7225435; PIDN:AAF40672.1; PID:g722543
A:Cross-references: GB:AE002379; GB:AE002098; NID:g7225435; PIDN:AAF40672.1; PID:g722543
B:Parkhili, J:, Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A:Aitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A:Accession: C81996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-504 < PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83367.1; PID:g737882
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Furuta, S.; Hayashi, H.; Hijikata, M.; Miyazawa, S.; Osumi, T.; Hashimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 313-317, 1986
A;Title: Complete nucleotide sequence of cDNA and deduced amino acid sequence of rat liv
A;Reference number: A25965; MUID:86094381
A;Accession: A25965
                                                                                                                                                                                                                                      Λ
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: D81224; C81996
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Reference number: A81000; MUID:20175755
A;Accession: D81224
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-527 <NAK>
A; Residues: 1-527 <NAK>
A; Cross-references: GB:M25680; GB:M23742; NID:g203333; PIDN:AAB42378.1; PID:g203335
A; Cross-references: GB:M25680; GB:M23742; NID:g203333; PIDN:AAB42378.1; PID:g203335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalase (EC 1.11.1.6) - rat
N.Alternate names: hydrogen peroxidase; hydrogen peroxide oxidoreductase
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: 18-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 03-Mar-2000
C.Saccession: JU0065; A25965; IS2202
R.Nakashima, H.; Yamamoto, M.; Goto, K.; Osumi, T.; Hashimoto, T.; Endo, H. Gene 79, 279-288, 1989
A.Fitle: Isolation and characterization of the rat catalase-encoding gene, A.Reference number: JU0065; MuID:90006757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:M11670; NID:g203344; PIDN:AAA40884.1; PID:g203345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: katA; NMB0216; NMA0050
C;Superfamily: catalase
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;59,99,132/Active site: His, Thr, Asm #status predicted
F;342/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riosumi, T.; Ozasa, H.; Miyazawa, S.; Hashimoto, T. Babochem. Biophys. Res. Commun. 122, 831-837, 1984 A;Title: Molecular cloning of cDNA for rat liver catalase. A;Reference number: 152202; MUID:84280086 A;Accession: 152202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 GAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-527 <FUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQ
```

ö

```
probable catalase (EC 1.11.1.6) [imported] - Sinorhizobium meliloti (strain 1021) mag C; Species: Sinorhizobium meliloti
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 14-Sep-2001
C; Accession: B95843
E; Pinan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her Proc. Natl. Acad. Sci. Us.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb psymb megaplasmid from the N2-fixing e A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: B95843
A; Accession: B95843
A; Accession: B95843
A; Residues: 1-705 < KUR;
A; Mesidues: 1-705 < KUR;
A; Cross-references: GB:AL591985; PIDN:CAC48410.1; PID:g15139882; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid psymb
B; Galibert, F.; Finan, T.W.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
C; Genetics: annotation
C; Genetics:
C; Genetics:
C; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein ycji [imported] - Lactococcus lactis subsp. lactis (strain IL140 C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C; Accession: C68662 R: Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
                        C; Accession: S49465
R; Henkle-Duehrsen, K.J.
submitted to the EMBL Data Library, October 1994
A; Reference number: S49452
A; Reference number: S49465
A; Accession: S49465
A; Accession: S49465
A; Rolecule type: mRNA
A; Residence: 1-482 < HENA
A; Residence: 1-482 < HENA
A; Coss-references: EMBL: X82176; NID: 9558624; PIDN: CAA57666.1; PID: 9558625
C; Superfamily: catalase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
C; S5,94,128/Active site: His, Ser, Asn #status predicted
F; 55,94, Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              39.5%; Score 62; DB 2; Length 482; 61.9%; Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%;
61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 TTAFGAPVWDDNNVITAGPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.5
Best Local Similarity 61.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: catC; SMb20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C86662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalase (EC 1.11.1.6) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 0.1 Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AD3621
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        per
                                                                                                                                                                                                                     C; Species: Brucella abortus
C; Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 04-Mar-2000
C; Accession: A55227
R; Sha, Z.; Stabel, T.J.; Mayfield, J.E.
A; Bacteriol. 176, 7375-7377, 1994
A; Title: Brucella abortus catalase is a periplasmic protein lacking a standard signal a; Reference number: A55227; MUID:95050323
A; Accession: A55227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: catalase (Reywords: chromoprotein; heme; homotetramer; iron; metalloprotein; oxidoreductase; 12-499/Product: catalase #status experimental <MAT> (15,93,127/Active site: His, Ser, Asn #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AD3621
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-507 <KUR>
A; Residues: 1-507 <KUR>
A; Cross-references: GB: AE008918; PIDN: AAL54135.1; PID: g17985098; GSPDB: GN00191
A; Experimental source: strain 16M
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-499 < CSHA>
A; Residues: 1-499 < CSHA>
A; Cross-references: GB:U11439; NID:g508707; PIDN:AAA64655.1; PID:g508708
C; Superfamily: catalase
C; Superfamily: catalase
C; Superfamily: catalase # theme; homotetramer; iron; metalloprotein; oxic
F; 2-499/Product: catalase # status experimental < MAXP.
F; 5-499/Product: catalase # status experimental < MAXP.
F; 5-5,93,127/Active site: His, Ser, Asn # status predicted
F; 337/Binding site: heme iron (Tyr) (axial ligand) # status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catalase (EC 1.11.1.6) - nematode (Onchocerca volvulus)
C;Species: Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 2
Pred. No. 0.23;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63;
Pred. No.
                                                                                                                                                                                                               catalase (EC 1.11.1.6) - Brucella abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 TTAFGAPVWDDNNVITAGPRG 29
                                     9 TTAFGAPVWDDNNVITAGPRG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TISAGAPIPDNONSLTAGERG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.18;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 12; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: catalase
Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: II
C; Superfamily: cata
C; Keywords: oxidore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: BMEII0893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S49465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                          셤
         ò
```

```
1;
A; Reference number: A86625; MUID:21235186; PMID:11337471
A; Accession: C86662
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-349 <STO>
A; Cross references: GB:AE005176; PID:912723163; PIDN:AAK04397.1; GSPDB:GN00146
A; Experimental source: strain IL1403
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Cross references: CG-A; Cross references: A; Cross references: Cross references: A; Cross references: Cross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.2%; Score 60; DB 2; Length 349; Best Local Similarity 56.5%; Pred. No. 0.42; Matches 13; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
```

Search completed: August 22, 2002, 07:46:14 Job time: 192 sec